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132260

mg

From: Huff, Sheela  
Sent: Monday, September 13, 2004 5:58 AM  
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Subject: search request for 10042347

Please search and interference search SEQ ID No. 4 of the above application.

Thanks

Sheela Huff  
Art Unit 1642  
571-272-0834  
Remsen 3A15  
mailbox Remsen 3C18

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

( Blank sheet )

GenCore version 5.1.6  
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# OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 18:25:17 ; Search time 78 Seconds

(without alignments)  
3884.656 Million cell updates/sec

Title: US-10-042-347-4

Perfect score: 546  
Sequence: 1 cacagccaccgagcttcca.....acagcttcacgacgctcc 546

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A COMB. seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B COMB. seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A COMB. seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B COMB. seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTCUS COMB. seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	546	100.0	546	US-09-315-689-4	Sequence 4, Appli
2	546	100.0	552	US-09-206-059-30	Sequence 30, Appli
3	546	100.0	563	US-09-231-077D-9	Sequence 9, Appli
4	546	100.0	3394	US-08-159-784-4	Sequence 4, Appli
5	534	97.8	534	US-09-315-689-4	Sequence 6, Appli
6	381.2	69.8	558	US-09-449-293-3	Sequence 3, Appli
7	381.2	69.8	558	US-09-775-325-3	Sequence 3, Appli
8	381.2	69.8	558	US-09-775-174-3	Sequence 3, Appli
9	381.2	69.8	565	US-08-985-526-37	Sequence 37, Appli
10	381.2	69.8	573	US-09-561-500-12	Sequence 12, Appli
11	381.2	69.8	573	US-09-561-108-12	Sequence 12, Appli
12	381.2	69.8	573	US-09-561-526-12	Sequence 12, Appli
13	381.2	69.8	573	US-09-561-459-12	Sequence 12, Appli
14	381.2	69.8	573	US-09-998-831-12	Sequence 12, Appli
15	381.2	69.8	620	US-09-231-077D-5	Sequence 5, Appli
16	379.6	69.5	568	US-09-231-077D-8	Sequence 8, Appli
17	379.6	69.5	580	US-09-231-077D-7	Sequence 7, Appli
18	379.6	69.5	4031	US-08-159-784-1	Sequence 1, Appli
19	378	69.2	582	US-09-231-077D-6	Sequence 6, Appli
20	60	11.0	79	US-09-231-077D-4	Sequence 4, Appli
21	57	10.4	71	US-09-231-077D-3	Sequence 3, Appli
22	46.6	8.5	1467	US-09-252-991A-1632	Sequence 1632, Ap
23	46.6	8.5	2025	US-09-252-991A-1536	Sequence 1536, Ap
24	46	8.4	1038	US-09-252-991A-9197	Sequence 9197, Ap
25	46	8.4	1410	US-09-252-991A-8867	Sequence 8867, Ap
26	46	8.4	2067	US-09-252-991A-9114	Sequence 9114, Ap
27	46	8.4	2634	US-09-252-991A-8976	Sequence 8976, Ap

28	45.6	8.4	2451	US-09-252-991A-7534	Sequence 7534, Ap
29	45.6	8.4	2661	US-09-252-991A-7807	Sequence 7807, Ap
30	45.6	8.4	2868	US-09-252-991A-7683	Sequence 7683, Ap
31	45.4	8.3	498	US-09-252-991A-15905	Sequence 15905, A
32	45.4	8.3	522	US-09-252-991A-15788	Sequence 15788, A
33	45.4	8.3	1101	US-09-252-991A-15814	Sequence 15814, A
34	45.4	8.3	1887	US-09-252-991A-15843	Sequence 15843, A
35	45.4	8.3	2103	US-09-252-991A-15876	Sequence 15876, A
36	44.8	8.2	1206	US-09-252-991A-3867	Sequence 3867, Ap
37	44.8	8.2	1320	US-09-252-991A-3779	Sequence 3779, Ap
38	44.4	8.1	1116	US-09-252-991A-2102	Sequence 2102, Ap
39	44.4	8.1	1224	US-09-252-991A-1793	Sequence 1793, Ap
40	44.4	8.1	3113	US-09-894-998A-52	Sequence 52, Appl
41	44	8.1	3350	US-09-894-998A-48	Sequence 48, Appl
42	43.6	8.0	1686	US-08-648-657-14	Sequence 14, Appl
43	43.6	8.0	1794	PCT-US95-14418-3	Sequence 3, Appli
44	43.6	8.0	1794	PCT-US95-15327-3	Sequence 3, Appli
45	43.6	8.0	2499	US-09-758-282B-94	Sequence 94, Appl

## ALIGNMENTS

RESULT 1  
US-09-315-689-4  
Sequence 4, Application US/09315689  
Patent No. 6346510  
GENERAL INFORMATION:  
APPLICANT: Folkman, Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions  
FILE REFERENCE: 05213-0229  
CURRENT APPLICATION NUMBER: US/09/315, 689  
CURRENT FILING DATE: 1999-05-20  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 546  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-315-689-4

Query Match 100.0%; Score 546; DB 4; Length 546;  
Best Local Similarity 100.0%; Pred. No. 8.1e-113;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CACAGCCACCGGACCTTCCAGCCGAGTGCCTCACTGTTGGCTCAACAGCCCTGTCA	60
DB	1	CACAGCCACCGGACCTTCCAGCCGAGTGCCTCACTGTTGGCTCAACAGCCCTGTCA	60
QY	61	GCGCGCATGCGGCGCATCCGCGGAGCCGACCTTCCAGTCTTCCAGCAGGCGCGGCGT	120
DB	61	GCGCGCATGCGGCGCATCCGCGGAGCCGACCTTCCAGTCTTCCAGCAGGCGCGGCGT	120
QY	121	GCGCGCATGCGGCGCATCCGCGGAGCCGACCTTCCAGTCTTCCAGCAGGCGCGGCGT	180
DB	121	GCGCGCATGCGGCGCATCCGCGGAGCCGACCTTCCAGTCTTCCAGCAGGCGCGGCGT	180
QY	181	GCGCGCATGCGGCGCATCCGCGGAGCCGACCTTCCAGTCTTCCAGCAGGCGCGGCGT	240
DB	181	GCGCGCATGCGGCGCATCCGCGGAGCCGACCTTCCAGTCTTCCAGCAGGCGCGGCGT	240
QY	241	CCAGCTGAGGAGGCTCTGTTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA	300
DB	241	CCAGCTGAGGAGGCTCTGTTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA	300
QY	301	TTTCTCTTTTCAAGGAGGAGCTCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCA	360
DB	301	TTTCTCTTTTCAAGGAGGAGCTCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCA	360
QY	361	CATGCTCGAGACCCCAAGCGGCGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAG	420
DB	361	CATGCTCGAGACCCCAAGCGGCGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAG	420

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RESULT 2
US-09-206-059-30
Sequence 30, Application US/09206059
Patent No. 6201104
GENERAL INFORMATION:
APPLICANT: Macdonald, Nicholas
APPLICANT: Sim, Kim Lee
TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and
FILE REFERENCE: 05213-0370
CURRENT APPLICATION NUMBER: US/09/206,059
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-206-059-30

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QY	541	GCCTCC	546	
Db	541	GCCTCC <td>546</td> <td></td>	546	
QY	541	GCCTCC <td>546</td> <td>     </td>	546	
Db	541	GCCTCC <td>546</td> <td></td>	546	

## RESULT 4

US-08-159-784-4  
: Sequence 4, Application US/08159784  
: Patent No. 5643783  
:  
: GENERAL INFORMATION:  
: APPLICANT: Bjorn R. Olsen  
: TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF  
: NUMBER OF SEQUENCES: 9  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Fish & Richardson  
: STREET: 225 Franklin Street  
: CITY: Boston  
: STATE: Massachusetts  
: COUNTRY: U.S.A.  
: ZIP: 02110-2804  
:  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
: COMPUTER: IBM PS/2 Model 502 or 55SX  
: OPERATING SYSTEM: MS-DOS (Version 5.0)  
: SOFTWARE: Wordperfect (Version 5.1)  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/159,784  
: FILING DATE: December 1, 1993  
: CLASSIFICATION: 530  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: John F. Freeman  
: REGISTRATION NUMBER: 29,066  
: REFERENCE/DOCKET NUMBER: 00246/170001  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (617) 542-5070  
: TELEFAX: (617) 542-8906  
: TELEX: 200154  
: INFORMATION FOR SEQ. ID NO.: 4:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 3394  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
:  
US-08-159-784-4

	Query Match	100.0%;	Score 546;	DB 1;	Length 3394;	
	Best Local Similarity	100.0%;	Pred. No. 1e-112;			
	Matches 546;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
QY	1	CACAGCCACCGGACATTTCAGCCGGGTCTCAACTGTGTGCGTCAACAGCCCCCTCTCA	60			
Db	1504	CACAGCCACCGGACATTTCAGCCGGGTCTCAACTGTGTGCGTCAACAGCCCCCTCTCA	1563			
QY	61	GGCAGCATGGGAGCATTCCGGGGGCCAATTCAGTGCTTCAGCAGGCGCGGCGCTG	120			
Db	1564	GGCAGCATGGGAGCATTCCGGGGGCCAATTCAGTGCTTCAGCAGGCGCGGCGCTG	1623			
QY	121	GGGCTGCGGGGACATCTTCCGCGCTTCTGTCTCGCGCTTGCAGACTCTTAACAGATC	180			
Db	1624	GGGCTGCGGGGACATCTTCCGCGCTTCTGTCTCGCGCTTGCAGACTCTTAACAGATC	1683			
QY	181	GTGCGCGGTTCGACC GGCGAGCCGTGCCATCGTCAACTCAAGAGCGAGGCTGTGTTT	240			
Db	1684	GTGCGCGGTTCGACC GGCGAGCCGTGCCATCGTCAACTCAAGAGCGAGGCTGTGTTT	1743			
QY	241	CCCAGCTGGAGAAGCTTTCTTCAGAGCTCTAAGAGTCCGCTGAAGCCCGGGGACAAGATC	300			
Db	1744	CCCAGCTGGAGAAGCTTTCTTCAGAGCTCTAAGAGTCCGCTGAAGCCCGGGGACAAGATC	1801			
QY	301	TTCCTCTTTAGAGGCAAGAGCGTCTGAAGGACACCCACCTGGCGCCAGAAAGACGTGTGG	360			
Db	1804	TTCCTCTTTAGAGGCAAGAGCGTCTGAAGGACACCCACCTGGCGCCAGAAAGACGTGTGG	1866			
QY	361	CATGCTCGACCCCAAGGGCGAGAGCTGACCGAGAGCTAATTGTGAGCGTGGCGACG	420			

## RESULT 5

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US-09-315-689-6
; Sequence 6, Application US/09315689
; Patent No. 6346510
;
; GENERAL INFORMATION:
; APPLICANT: Polkman, Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
; FILE REFERENCE: 05213-0229
; CURRENT APPLICATION NUMBER: US/09/315,689
; CURRENT FILING DATE: 1999-05-20
;
; NUMBER OF SEQ ID NOS: 6
;
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 6
;
; LENGTH: 534
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
US-09-315-689-6

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	Query Match	97.8%	Score 534	DB 4	Length 534	
	Best Local Similarity	100.0%	Pred. No. 3.7e-110			
	Matches 534	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	13	GACTTCAGACGGGTGCTCCACCTGGTGTGCGTCAACAGCCCTCTTCAGGCGGACATGCGG	72			
DB	1	GACTTCAGACGGGTGCTCCACCTGGTGTGCGTCAACAGCCCTCTTCAGGCGGACATGCGG	60			
QY	73	GGCATCCGGGGGGCCGACCTTCACATGTCTTCCAGTAAGGCGCGGCGCGGCGGCGGCGG	132			
DB	61	GGCATCCGGGGGGCGAATTCCAGTGTCTTCAGAGAGCGCGGCGCGGCGGCGGCGGCGG	120			
QY	133	ACCTTCGGGGCTTCCTGTCTCGGCGCTTCGAGGACCTGTACAGATCGTGCGCGCTGCC	192			
DB	121	ACCTTCGGGGCTTCCTGTCTCGGCGCTTCGAGGACCTGTACAGATCGTGCGCGCTGCC	180			
QY	193	GACGCGCAGACGTCGCCCATCTGTCAACCTCAAGGACGAGCTGTGTTCCTCCAGCTGGAG	252			
DB	181	GACGCGCAGACGTCGCCCATCTGTCAACCTCAAGGACGAGCTGTGTTCCTCCAGCTGGAG	240			
QY	253	GCTCTGTTCTCAGGCTCTGAGGGTTCGGCTGAAAGCCCGGGGACAGATCTTCCTCTTAC	312			
DB	241	GCTCTGTTCTCAGGCTCTGAGGGTTCGGCTGAAAGCCCGGGGACAGATCTTCCTCTTAC	300			
QY	313	GGCAAGGACGTCCTCGTAGGACCCACATCGGCCGACGAAGAGGTGTGGCATGTGCTGGAC	372			
DB	301	GGCAAGGACGTCCTCGTAGGACCCACATCGGCCGACGAAGAGGTGTGGCATGTGCTGGAC	360			
QY	373	CCCAACGGGCGCAGGCTGACCGAGAGCTTACTGTGAGCGTGTGGCGAGCGAGGCTCCTTG	433			
DB	361	CCCAACGGGCGCAGGCTGACCGAGAGCTTACTGTGAGCGTGTGGCGAGCGAGGCTCCTTG	420			
QY	433	GGCACGGGCGAGGCTCTCGCTGTCTGTGGGGGGCAGGCTCCTGTGGGCGAGAGGCGCGAGC	492			
DB	421	GGCACGGGCGAGGCTCTCGCTGTCTGTGGGGGGCAGGCTCCTGTGGGCGAGAGGCGCGAGC	480			
QY	493	TGGCATACGCGTACATCGTGTCTGTGATTTGAGAGACGTTTATACATCTGCTCC	546			
DB	481	TGGCATACGCGTACATCGTGTCTGTGATTTGAGAGACGTTTATACATCTGCTCC	534			

```

RESULT 7
US-09-775-325-3
; Sequence 3, Application US/0975325
; Patent No. 6500449
; GENERAL INFORMATION:
; APPLICANT: Abitbol, Marc
; APPLICANT: Uleza, Yves
; APPLICANT: Menasche, Maurice
; APPLICANT: Bossard, Carine
; APPLICANT: Van Den Bergh, Loic
; APPLICANT: Bonnel, Sebastian
; APPLICANT: Prats, Hervé
; APPLICANT: Honiger, Jiri
; APPLICANT: Neuner-Jehle, Martin
; TITLE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
; FILE REFERENCE: 8076.202USD1
; CURRENT APPLICATION NUMBER: US/09/775.325
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US 09/449,293
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Rattus rattus
; US-09-775-325-3

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Query Match	95.8%;	Score 381.2;	DB 4;	Length 558;
Best Local Similarity	61.1%;	Pred. No. 3.1e-76;		
Matches	443;	Conservative	0;	Mismatches 103; Indels 0; Gaps 0;
QY	1	CACAGCCACCGGCATCTTCCAGCCGAGTCTCCACCTGTGGAGCTCAACAGCCCCCTGTCA	60	
Db	4	CATACCTCATCAGAGCTTTTCAGCCAGTGTCTCCACCTGTGGAGCTCAACAGCCCCCTGTCT	63	
QY	61	GGCGGCATCGCGGGGCATTCGCGGGGCCGACTTCCAGTGTCTTCCAGAGGCGCGGACCGTG	120	
Db	64	GGAGGCATCGGTGTATCCGTGGAGAGATTTCCAGTGTCTTCCAGCAGACCCGACCGGCGTG	123	
QY	121	GGGCTGGGCGGACCTTCCGCGCCTTCCTGTCTCGCGCCGACGAGGACCTGTACAGATTC	180	
Db	124	GGGCTGTGGGCACCTTCCGCGCCTTTCCTGTCTCTGTAGGCTGAGGATTCATAGCATTC	183	
QY	181	GTGCGCGGTCCGACCGCGCAGCCGATGCCATCGTCAACTCAAGGACGAGCTGTGTTT	240	
Db	184	GTGCGCGGTCTGACCGGCGGAGTCTGTGCCATCGTCAACTCAAGGACGAGGTGTATCT	243	
QY	241	CCGACGTGGGAGGCTGTCTTCTCAGAGCTGTAGGGTCCGCTGAAGCCCGGGGACCGATTC	300	
Db	244	CCGACGTGGGACTTCCTGTCTTCTGAGCTCCGAGGATCACTGACACCGGGGCGCGGATTC	303	
QY	301	TTCTCTTTTTCAGGCAAGAGCGTCTGAGGACCCCACTGGCCCCAGAGAGGTGTG	360	
Db	304	TTTTCTTTTTCAGGCGAGAGATGTCTGAGAACCCCACTGGCCCCAGAGAGCGTATGG	363	
QY	361	CATGCTTCGGAATCCCAACGGGCGCAGGTTCACGAGAGCTATGTGACGCTGGCGAGCG	420	
Db	364	CACGCTTCGGAATCCCAAGGGCGGAGGCTGTATGAGAGGTATCTGTGAGCATGGCGAATC	423	
QY	421	GAGGCTCCCTCCGSCCAGGGGCGAGGCTCTCTCGTGTGGGGGGGAGGCTCTCGGGGACG	480	
Db	424	GAAACTCTCGGGCTTACAGGCTCAGGCTCTCTCTCTCTGTCTGTGAGGAGGCTCTCGAAGC	483	
QY	481	AATGCGCGAGCTGCATCAAGCTTACATCTGTGCTTCGATTTGAAGACAGCTTCATGACT	540	
Db	484	AAAGCTCGAGGCTGCACAAAGCTTACATCTCTGTGTGATTTGAGATATCTTCATGACC	543	
QY	541	GGCTCC 546		
Db	544	TCTTTC 549		

## RESULT 8

US-09-775-174-3  
 ; Sequence 3, Application US/09775174  
 ; Patent No. 6663894  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Adilbol, Marc  
 ; APPLICANT: Uteza, Yves  
 ; APPLICANT: Menasche, Maurice  
 ; APPLICANT: Boscard, Carine  
 ; APPLICANT: Van Den Bergh, Loic  
 ; APPLICANT: Bonnel, Sebastian  
 ; APPLICANT: Prats, Hervé  
 ; APPLICANT: Honiger, Jiri  
 ; APPLICANT: Neuner-Jehle, Martin  
 ; TITLE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS  
 ; FILE REFERENCE: 8076.202USD2  
 ; CURRENT APPLICATION NUMBER: US/09/775,174  
 ; CURRENT FILING DATE: 2001-02-01  
 ; PRIOR APPLICATION NUMBER: US 09/449,293  
 ; PRIOR FILING DATE: 1999-11-24  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 558  
 ; TYPE: DNA  
 ; ORGANISM: Rattus rattus  
 ; US-09-775-174-3

Query Match 69.8%; Score 381.2; DB 4; Length 558;  
 Best Local Similarity 81.1%; Pred. No. 3.1e-76;  
 Matches 443; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

1 CACAGCCACCGGACCTTCCAGCCGGGTCTCACTGTTGGGCTCAACAGCCCTCTGCA 60  
 4 CATACTATGAGACTTTTACGACATGCTCACTGATGAGCACTGAACACCCCTGTCT 63  
 61 GAGCGCATGCGGGGCAATCGCGGGGCGCACTTCAGTGTCTTCAAGCGGGCGGGCGTG 120  
 64 GAGGCGATGCGGTATCCGTGAGACAGATTTCAGATGCTTCCAGCAAGCCGAGCCGTG 123  
 121 GGGCTGGGGGCACTTTCGGCGCTTCTGTCTTCCGCGCTGCAAGACCTGTACAGCATC 180  
 124 GGGCTGTGGGCACTTTCGGCGCTTCTGTCTTCCAGCTGCAAGATCTTATAGCATC 183  
 181 GGGCGCGTCCACCGCGGAGCGTCCCATGTCATCACTTCAAGACGAGCTGTGTT 240  
 184 GTGCGCGTGTGACCGGGGCTCTGTCCCATGTCATCACTTGAAGACGAGTGTATCT 243  
 241 CCCAGCTGGAGGCTCTGTTCTCAAGCTCTGAAGGATCGCTGAAGCCCGGGGCGCATC 300  
 244 CCCAGCTGGAGCTCCCTGTTTCTGTCCCGAGGATCACTTGAAGCCCGGGGCGCATC 303  
 301 TTCTCCTTTGACGGCAAGAGCTCTTGAAGGACCCCACTTGGCCCGCAAGAGCTGTG 360  
 304 TTTTCTTTTGAAGCGCAGAGATGTCCTGAAGACCCAGCTTGGCGCAAGAGCTGTG 363  
 361 CATGCTGGAGCCCAACCGGGGCGAGCTGACCGAGACTACTGTGAGAGCTGTGAGAG 420  
 364 CAGGCTGGAGCCCAACCGGGGCGAGCTGATGAGAGATTTACTGTGAGAGCATGAGCA 423  
 421 GAGGCTCCCTCGAGCAGGAGGCTCTCTGCTGCTGAGGGGAGAGGCTCTCTGAGGAG 480  
 424 GAACTACTGGGGCTAAGGTCAAGGCTCTCTCTGCTGCTGAGGAGGCTCTGAGAGAG 483  
 481 AGTCCCGGAGCTGCTCAATACGCTTACATGTGTCTGATTTGAGAACTACTTCAATG 540  
 484 AAGCTGCGAGCTGCAACAGCTACATGCTCTGTGATTTGAGAACTACTTCAATG 543  
 541 GCGTCC 546  
 544 TCTTTT 549

## RESULT 9

US-08-985-526-37  
 ; Sequence 37, Application US/08985526  
 ; Patent No. 6080728  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mixson, James A  
 ; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA  
 ; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE  
 ; TITLE OF INVENTION: THERAPY  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: Connolly, Boye, Lodge, & Hurtz  
 ; STREET: 1220 Market Street, P.O. Box 2207  
 ; CITY: Wilmington  
 ; STATE: Delaware  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19899

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/985,526  
 FILING DATE:  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/608,845  
 FILING DATE: 16-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McMorrow Jr., Robert G  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (302) 658-9141  
 TELEFAX: (302) 658-5613  
 INFORMATION FOR SEQ ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 565 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-985-526-37

Query Match 69.8%; Score 381.2; DB 3; Length 565;  
 Best Local Similarity 81.1%; Pred. No. 3.1e-76;  
 Matches 443; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

1 CACAGCCACCGGACCTTCCAGCCGGGTCTCACTGTTGGGCTCAACAGCCCTCTGCA 60  
 11 CATACTATGAGACTTTTACGACATGCTCACTGATGAGCACTGAACACCCCTGTCT 70  
 61 GAGCGCATGCGGGGCAATCGCGGGGCGCACTTCAGTGTCTTCAAGCGGGCGGGCGTG 120  
 71 GAGGCGATGCGGTATCCGTGAGACAGATTTCAGATGCTTCCAGCAAGCCGAGCCGTG 130  
 121 GGGCTGGGGGCACTTTCGGCGCTTCTGTCTTCCGCGCTGCAAGACCTGTACAGCATC 180  
 124 GGGCTGTGGGCACTTTCGGCGCTTCTGTCTTCCAGCTGCAAGATCTTATAGCATC 190  
 181 GTGCGCGTGTGACCGGGGCTCTGTCCCATGTCATCACTTCAAGACGAGCTGTGTT 240  
 191 GTGCGCGTGTGACCGGGGCTCTGTCCCATGTCATCACTTGAAGAGAGAGTGTATCT 250  
 241 CCCAGCTGGAGGCTCTGTTCTCAAGCTCTGAAGGATCGCTGAAGCCCGGGGCGCATC 300  
 251 CCCAGCTGGAGCTCCCTGTTTCTGTCCCGAGGATCACTTGAAGCCCGGGGCGCATC 310  
 301 TTCTCCTTTGACGGCAAGAGCTCTTGAAGGACCCCACTTGGCCCGCAAGAGGCTGTG 360  
 311 TTTTCTTTTGAAGCGCAGAGATGTCCTGAAGACCCAGCTTGGCGGAGAGGCTATG 370  
 361 CATGCTGGAGCCCAACCGGGGCGAGCTGACCGAGAGCTACTGTGAGAGCTGTGAGAG 420  
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[illegible]

442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Db 442 GAACTACTGGGCTACAGGTCAGGCTCCTCCCTGCTGTCAGGCAGGCTCCTGGAACAG 501





OY 541 GCCTCC 546  
Db 562 TCCTTC 567

RESULT 14  
US-09-998-831-12  
Sequence 12, Application US/09998831  
Patent No. 6676941  
GENERAL INFORMATION:  
APPLICANT: Philip E. Thorpe  
APPLICANT: Rolf A. Breken  
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY  
TITLE OF INVENTION: INHIBITING VEGF  
FILE REFERENCE: 4001.002584  
CURRENT APPLICATION NUMBER: US/09/998.831  
CURRENT FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 09/561,108  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 573  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
NAME/KEY: CDS  
LOCATION: (1)..(573)  
US-09-998-831-12

Query Match 69.8%; Score 381.2; DB 4; Length 573;  
Best Local Similarity 81.1%; Pred. No. 3.2e-76;  
Matches 443; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

OY 1 CACAGCCACCGGACTTCCAGCGGCTGCTCCAGCTGTTGGGCTCAACAGCCCTCTGCA 60  
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Db 82 GGAGGCAATGCGTGTATCCGTGAGAGATTTCCAGTGTCTTCCAGAGGCGCGCGCTG 141  
OY 121 GGGCTGGGGGCACTTCCGCGGCTTCTGCTGCTGCGCGGCGAGGCTGTACAGCATC 180  
Db 142 GGGCTGTGGGCACTTCCGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 201  
OY 181 GTGCGCGTGGCGACCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
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OY 241 CCGAGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
Db 262 CCGAGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 321  
OY 301 TTCTCTTTTGAAGGAGAGAGTCTGAGAGACCCAGCTGCGCGGCGAGAGAGCTGTGG 360  
Db 322 TTCTCTTTTGAAGGAGAGAGTCTGAGAGACCCAGCTGCGCGGCGAGAGAGCTGTGG 381  
OY 361 CATGCTCGAGCCCAAGGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 420  
Db 382 CAGGCTCGAGCCCAAGGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 441  
OY 421 GAGGCTCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 480  
Db 442 GAACTACTGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 501  
OY 481 AGTGGCGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 540  
Db 502 AAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 561

OY 541 GCCTCC 546  
Db 562 TCCTTC 567

RESULT 15  
US-09-231-077D-5  
Sequence 5, Application US/09231077D  
Patent No. 6651098  
GENERAL INFORMATION:  
APPLICANT: Harding, E.I.  
APPLICANT: Violand, B.N.  
TITLE OF INVENTION: Method of producing mouse and human  
TITLE OF INVENTION: endostatin  
FILE REFERENCE: S03071-00-US  
CURRENT APPLICATION NUMBER: US/09/231.077D  
CURRENT FILING DATE: 1999-01-14  
PRIOR APPLICATION NUMBER: 60/075,587  
PRIOR FILING DATE: 1998-02-23  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 620  
TYPE: DNA  
ORGANISM: human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(620)  
OTHER INFORMATION: n = A,T,C or G  
US-09-231-077D-5

Query Match 69.8%; Score 381.2; DB 4; Length 620;  
Best Local Similarity 81.1%; Pred. No. 3.2e-76;  
Matches 443; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

OY 1 CACAGCCACCGGACTTCCAGCGGCTGCTCCAGCTGTTGGGCTCAACAGCCCTCTGCA 60  
Db 15 CATACTCATGAGACTTTTGAAGCAGTGTCTCCAGCTGTGAGCACTGAAACCCCTCTGCT 74  
OY 61 GCGGCGATGCGGGGCACTCCGCGGGCCGACTTCCAGTGTCTTCCAGAGGCGCGCGCTG 120  
Db 75 GGAGGCAATGCGTGTATCCGTGAGAGATTTCCAGTGTCTTCCAGAGGCGCGCGCTG 134  
OY 121 GGGCTGGGGGCACTTCCGCGGCTTCTGCTGCTGCGCGGCGAGGCTGTACAGCATC 180  
Db 135 GGGCTGTGGGCACTTCCGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194  
OY 181 GTGCGCGTGGCGACCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
Db 195 GTGCGCGTGGCGACCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254  
OY 241 CCGAGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
Db 255 CCGAGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314  
OY 301 TTCTCTTTTGAAGGAGAGTCTGAGAGACCCAGCTGCGCGGCGAGAGAGCTGTGG 360  
Db 315 TTCTCTTTTGAAGGAGAGTCTGAGAGACCCAGCTGCGCGGCGAGAGAGCTGTGG 374  
OY 361 CATGCTCGAGCCCAAGGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 420  
Db 375 CAGGCTCGAGCCCAAGGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 434  
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OY 481 AGTGGCGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 540  
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Db 555 TCTTC 560

Search completed: September 15, 2004, 20:12:14  
Job time : 80 secs

(D/h/18 Sept)

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 18:07:50 ; Search time 2452 Seconds

(without alignments)  
6649.572 Million cell updates/sec

Title: US-10-042-347-4

Perfect score: 546  
Sequence: 1 cacagccacagcgcagcttcca.....acagctcatgacgcctcc 546

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

EST.\*  
1: em\_estba.\*  
2: em\_estbm.\*  
3: em\_estin.\*  
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5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rtd.\*  
26: em\_gss\_pig.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	546	100.0	707	10	BE908201
2	546	100.0	757	10	BE906253
3	546	100.0	881	14	CD105862
4	546	100.0	4230	11	BC063833

5	519	95.1	944	13	B0859398
6	508.6	92.2	929	13	B0672290
7	504.2	92.3	703	13	B0615520
8	495	90.7	682	9	AM089583
9	490	89.7	683	12	BM683067
10	487.2	89.2	832	12	BG387051
11	485.2	88.9	979	13	B0673186
12	476	87.2	884	12	B161007
13	474.2	86.8	618	9	AV696242
14	469.4	86.0	1093	13	B0723254
15	463	83.0	664	13	B0632049
16	453	83.0	715	9	AU125614
17	451.4	82.7	947	13	B0556872
18	450.6	82.5	745	10	AM243446
19	445	81.5	639	12	BM983137
20	443.4	81.2	634	13	B0772348
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22	440.8	80.7	660	10	AM192502
23	438.4	80.3	717	9	A1890773
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25	434	79.5	616	13	B0158380
26	425	77.8	726	9	A1814791
27	419.2	76.8	630	10	BE475568
28	418	76.6	645	10	BE621228
29	417.4	76.4	808	9	AM080065
30	412	75.5	605	12	BM998650
31	408.4	74.8	551	10	BE074455
32	406.2	74.4	577	10	BE046311
33	403.8	74.0	603	10	AM439633
34	394	72.2	680	9	AM090100
35	392.8	71.9	921	13	BX453476
36	391	71.6	443	9	AV698069
37	388	71.1	575	10	BE114979
38	387.4	71.0	504	14	CF789984
39	386.4	70.8	396	9	AV691878
40	386.4	70.8	402	9	AV689623
41	384.8	70.5	675	5	A1963657
42	381.2	69.8	843	10	BF385854
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45	380.2	69.6	715	14	CB596713

## ALIGNMENTS

RESULT 1  
LOCUS BE908201  
DEFINITION BE908201.1 GI:10402537  
ACCESSION BE908201  
VERSION BE908201  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 707)  
Nih-MGC http://mgc.nci.nih.gov/  
CONTACT Robert Strausberg, Ph.D.  
UNPUBLISHED (1999)  
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
plate: ILAM9704 row: d column: 16  
High quality sequence stop: 688.

## FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3902175"

/tissue\_type="epithelioid carcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Nct1; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."

## ORIGIN

Query Match 100.0%; Score 546; DB 10; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-85;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CACAGCCACCGCGACTTCCAGCGGTGCTCCACCTGTTGCGCTCAACAGCCCGCTGCA 60
Db 11 CACAGCCACCGCGACTTCCAGCGGTGCTCCACCTGTTGCGCTCAACAGCCCGCTGCA 70
QY 61 GCGCGCATGCGGGGCAATCCGCGGGGCGGACTTCCAGTGTTCAGCAAGCGCGGGCCGTG 120
Db 71 GCGCGCATGCGGGGCAATCCGCGGGGCGGACTTCCAGTGTTCAGCAAGCGCGGGCCGTG 130
QY 121 GGGCTGCGGCGCACTTCCGCGCTTCTCTGCGCGCTGCGAGACCTGTGAAGCATC 180
Db 131 GGGCTGCGGCGCACTTCCGCGCTTCTCTGCGCGCTGCGAGACCTGTGAAGCATC 190
QY 181 GTGCGCGGTGCGGCGGCGGCGGCTCCATGTCAACTCAAGAGAGAGCTGTGTTT 240
Db 191 GTGCGCGGTGCGGCGGCGGCGGCTCCATGTCAACTCAAGAGAGAGCTGTGTTT 250
QY 241 CCAGAGTGGAGAGGCTGTGTTCAAGGCTGAGAGGTTCCGTTGAAGGCTCCGGGCGAGCATC 300
Db 251 CCAGAGTGGAGAGGCTGTGTTCAAGGCTGAGAGGTTCCGTTGAAGGCTCCGGGCGAGCATC 310
QY 301 TTCTCTTTGACGCGCAAGAGAGTCTGAGGCAAGCCCACTGCGCCCGAGAAAGGCTGTGG 360
Db 311 TTCTCTTTGACGCGCAAGAGAGTCTGAGGCAAGCCCACTGCGCCCGAGAAAGGCTGTGG 370
QY 361 CATGCTCTGCAAGCCCAAGGCGGCAAGGCTGAGAGGATCTGTGAAGAGCTGTGCGAGC 420
Db 371 CATGCTCTGCAAGCCCAAGGCGGCAAGGCTGAGAGGATCTGTGAAGAGCTGTGCGAGC 430
QY 421 GAGGCTCCCTCGGCGCAAGGCGCTCTGCTGCTGCGGGGCGAGGCTCTTGGGGCAG 480
Db 431 GAGGCTCCCTCGGCGCAAGGCGCTCTGCTGCTGCGGGGCGAGGCTCTTGGGGCAG 490
QY 481 AGTGCAGCGAGCTGCAATCAAGCTTACATGCTGTGCTGTGCAATGAGAAAGCTTATAGCT 540
Db 491 AGTGCAGCGAGCTGCAATCAAGCTTACATGCTGTGCTGTGCAATGAGAAAGCTTATAGCT 550
QY 541 GCGCTCC 546
Db 551 GCGCTCC 556

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RESULT 2  
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 LOCUS 60150237FL NIH\_MGC\_70 Homo sapiens cDNA clone IMAGE:3904208 5',  
 DEFINITION mRNA sequence.  
 BE906253  
 BE906253.1 GI:10399595  
 ACCESSION  
 VERSION  
 KEYWORDS  
 EST.  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
 1 (bases 1 to 757)

## AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: ATCC

## JOURNAL

TITLE

COMMENT

CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.llnl.gov>  
 Plate: LIA9709 row: 1 column: 09

## FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3904208"

/tissue\_type="epithelioid carcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Nct1; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."

## ORIGIN

Query Match 100.0%; Score 546; DB 10; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-85;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CACAGCCACCGCGACTTCCAGCGGTGCTCCACCTGTTGCGCTCAACAGCCCGCTGCA 60
Db 36 CACAGCCACCGCGACTTCCAGCGGTGCTCCACCTGTTGCGCTCAACAGCCCGCTGCA 95
QY 61 GCGCGCATGCGGGGCAATCCGCGGGGCGGACTTCCAGTGTTCAGCAAGCGCGGGCCGTG 120
Db 96 GCGCGCATGCGGGGCAATCCGCGGGGCGGACTTCCAGTGTTCAGCAAGCGCGGGCCGTG 155
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Db 156 GGGCTGCGGCGCACTTCCGCGCTTCTCTGCGCGCTGCGAGACCTGTGAAGCATC 215
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QY 241 CCAGAGTGGAGAGGCTGTGTTCAAGGCTGAGAGGTTCCGTTGAAGGCTCCGGGCGAGCATC 300
Db 276 CCAGAGTGGAGAGGCTGTGTTCAAGGCTGAGAGGTTCCGTTGAAGGCTCCGGGCGAGCATC 335
QY 301 TTCTCTTTGACGCGCAAGAGAGTCTGAGGCAAGCCCACTGCGCCCGAGAAAGGCTGTGG 360
Db 336 TTCTCTTTGACGCGCAAGAGAGTCTGAGGCAAGCCCACTGCGCCCGAGAAAGGCTGTGG 395
QY 361 CATGCTCTGCAAGCCCAAGGCGGCAAGGCTGAGAGGATCTGTGAAGAGCTGTGCGAGC 420
Db 396 CATGCTCTGCAAGCCCAAGGCGGCAAGGCTGAGAGGATCTGTGAAGAGCTGTGCGAGC 455
QY 421 GAGGCTCCCTCGGCGCAAGGCGCTCTGCTGCTGCGGGGCGAGGCTCTTGGGGCAG 480
Db 456 GAGGCTCCCTCGGCGCAAGGCGCTCTGCTGCTGCGGGGCGAGGCTCTTGGGGCAG 515
QY 481 AGTGCAGCGAGCTGCAATCAAGCTTACATGCTGTGCTGTGCAATGAGAAAGCTTATAGCT 540
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QY 541 GCGCTCC 546
Db 576 GCGCTCC 581

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Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNU)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: WCC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNU at:  
<http://image.lnl.gov>  
Plate: NDAM424 row: g column: 24  
High quality sequence spot: 689.

## Location/Qualifiers

## Homo sapiens

## BC063833

M Homo sapiens

1 {base

Klausner  
Altschul

## USA

Tissue  
CDNA LibDNA Sequ  
BC Cance

Steven  
Susanna

Sen Lee,  
Ness, Pa

Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natsia van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18765747

## FEATURES

Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6181818"  
/tissue\_type="Peripheral Nervous System, dorsal root ganglion"  
/clone\_id="Lupski\_dorsal\_root\_ganglion"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"

## ORIGIN

Query Match 100.0%; Score 546; DB 11; Length 4230;  
Best Local Similarity 100.0%; Pred. No. 1.5e-84;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACACCCACCCGCACTTCCAGCGGCTGCTCCAGTGTGGCTTCAACACCCCTCTGCA 60  
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61 GCGCGCATGCGGGGCACTCCGCGGGGCGCACTCCAGTGTGGCTTCAACAGCGGGGCGGTG 120  
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3555 GCGCGCATGCGGGGCACTCCGCGGGGCGCACTCCAGTGTGGCTTCAACAGCGGGGCGGTG 3614  
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121 GCGCGCATGCGGGGCACTTCCGCGGCTTCTGCTGCTGCGCGCTTCAACAGCTTGAACAGATC 180  
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3615 GCGCGCATGCGGGGCACTTCCGCGGCTTCTGCTGCTGCGCGCTTCAACAGCTTGAACAGATC 3674  
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181 GCGCGCATGCGGGGCACTCCGCGGGGCGCACTCCAGTGTGGCTTCAACAGCGGGGCGGTG 240  
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3735 CCGAGCTGAGAGCTGTTCTCAGGCTTGAAGGCTCCGCTGAAGCCCGGGGCGCAAGCATC 3794  
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3795 TTCTCTTTGACGCGCAAGGACGTTCTGAGGACCCCACTGCGCCCAAGAGCGTGTGG 3854  
|||  
361 CAGGCTGAGAGCTCCCAAGCGGGGCGAGCTGACGAGGCTACTGAGAGCTGTGGGAGG 420  
|||  
3855 CAGGCTGAGAGCTCCCAAGCGGGGCGAGCTGACGAGGCTACTGAGAGCTGTGGGAGG 3914  
|||  
421 GAGGCTGAGAGCTCCCAAGCGGGGCGAGCTGAGGCTGAGGAGGAGGCTCTGAGGAGG 480  
|||  
3915 GAGGCTGAGAGCTCCCAAGCGGGGCGAGCTGAGGCTGAGGAGGAGGCTCTGAGGAGG 3974  
|||  
481 AGTGGCGGAGCTGCAATCAAGCTTCAATGAGCTGCTGATTTGAGAAAGAGCTTCAATGACT 540  
|||  
3975 AGTGGCGGAGCTGCAATCAAGCTTCAATGAGCTGCTGATTTGAGAAAGAGCTTCAATGACT 4034  
|||  
541 GCCTCC 546  
|||  
4035 GCCTCC 4040

RESULT 5  
B0859398/c  
LOCUS  
DEFINITION  
B0859398 944 bp mRNA linear EST 16-OCT-2002  
AGENCY: 10434549 NIH\_MGC\_109 Homo sapiens cDNA clone  
IMAGE: 6650260 5', mRNA sequence.

ACCESSION  
B0859398  
B0859398.1 GI:24044390  
EST.

## KEYWORDS

## SOURCE

## ORGANISM

## Homo sapiens (human)

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## 1 (bases 1 to 944)

NHL-MGC <http://mgi.nci.nih.gov/>

## Unpublished (1999)

## CONTACT: Robert Strausberg, Ph.D.

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

## Tissue Procurement: ATCC

## CDNA Library Preparation: Rubin Laboratory

## CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

## DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>

## Plate: LCM2895 row: d column: 04

## High quality sequence stop: 572.

## Location/Qualifiers

## 1..944

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /clone="IMAGE:6650260"

## /tissue\_type="teratocarcinoma, cell line"

## /lab\_host="DH10B (phage-resistant)"

## /clone\_id="NIH\_MGC\_109"

## /note="Organ: ovary; Vector: pOT7; Site 1: EcoRI; Site 2: XhoI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 95.1%; Score 519; DB 13; Length 944;  
Best Local Similarity 98.0%; Pred. No. 4.5e-80;  
Matches 536; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

1 CACAGCCACCGGCACTTCCAGCGGCTGCTCCAGTGTGGCTTCAACAGCCCTCTGTC 59  
|||  
712 CAGGCTGAGAGCTCCCAAGCGGGGCGAGCTGAGGCTACTGAGAGCTGTGGGAGG 653  
|||  
60 AGGCGCATGCGGGGCACTCCGCGGGGCGCACTCCAGTGTGGCTTCAACAGCGGGGCGGT 119  
|||  
652 AGGCGCATGCGGGGCACTCCGCGGGGCGCACTCCAGTGTGGCTTCAACAGCGGGGCGGT 593  
|||  
120 GAGGCTGAGAGCTCTTCCGCGGCTTCTGCTGCTGCGCGCTTCAACAGCTTGAACAGAT 179  
|||  
592 GAGGCTGAGAGCTCTTCCGCGGCTTCTGCTGCTGCGCGCTTCAACAGCTTGAACAGAT 533  
|||  
180 GAGGCTGAGAGCTCTTCCGCGGCTTCCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 239  
|||  
532 GAGGCTGAGAGCTCTTCCGCGGCTTCCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 473  
|||  
240 TCCAGCTGAGAGCTCTTCCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 299  
|||  
472 TCCAGCTGAGAGCTCTTCCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 413  
|||  
300 CTCTCTCTTTGACGCGCAAGGACGTTCTGAGGACCCCACTGAGGACCCCAAGAGAGGCTGTG 359  
|||  
412 CTCTCTCTTTGACGCGCAAGGACGTTCTGAGGACCCCACTGAGGACCCCAAGAGAGGCTGTG 353  
|||  
360 GCATGCTGAGAGCTCCCAAGCGGGGCGAGCTGACGAGGCTACTGAGAGAGTGTGGAGAG 419  
|||  
352 GCATGCTGAGAGCTCCCAAGCGGGGCGAGCTGACGAGGCTACTGAGAGAGTGTGGAGAG 293







RESULT 9  
 BM683067/c 683 bp mRNA linear EST 27-FEB-2002  
 LOCUS  
 DEFINITION UI-E-BO1-aj4-g-02-0-UI.s1 UI-E-BO1 Homo sapiens CDNA clone  
 ACCESSION BM683067  
 VERSION BM683067.1 GI:18992963  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PubMed 8889548  
 COMMENT  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this CDNA  
 sequence: 1-44, >POLY A#simple\_repeat (matched complement)  
 Seq primer: M13 Forward  
 POLYA=Yes.

FEATURES  
 source  
 1.683  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-BO1-aj4-g-02-0-UI"  
 /tissue\_type="fetal eye"  
 /dev\_stage="fetal"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-BO1"  
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker. Site 1: EcoR I; Site 2: Not I;  
 UI-E-BO1 is a normalized CDNA library containing the  
 following tissue(s): fetal eye. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand CDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded CDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand CDNA contains a library tag  
 (dT)18 tail. The sequence tag for this library is  
 CGGCTATACC. This library was created for the program, Gene  
 Discovery in the Visual System, supported by National Eye  
 Institute (NEI).  
 TAG\_TISSUE=human fetal eye  
 TAG\_LIB=UI-E-BO1  
 TAG\_SEQ=CGGCTATACC"

ORIGIN  
 Query Match 89.7%; Score 490; DB 12; Length 683;  
 Best Local Similarity 99.8%; Pred. No. 4.3e-75;  
 Matches 490; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 TGTACAGGCGGATCCGCGGCGCATCCGCGGCGCCGACCTTCAGTGTCTTCAGACGCGCGG 115  
 Db 683 TGTACAGGCGGATCCGCGGCGCATCCGCGGCGCCGACCTTCAGTGTCTTCAGACGCGCGG 624  
 QY 116 CCGTGGGCGCTGGCGGCGACCTTCGCGGCTTCCTGCTCGGCGCTGAGAGGAGGAGGAGG 175  
 Db 623 CCGTGGGCGCTGGCGGCGACCTTCGCGGCTTCCTGCTCGGCGCTGAGAGGAGGAGGAGG 564  
 QY 176 GCATCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 235  
 Db 563 GCATCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 504  
 QY 236 TGTTCCTCCAGTGGGAGGCTGTCTTCAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGG 295  
 Db 503 TGTTCCTCCAGTGGGAGGCTGTCTTCAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGG 444  
 QY 296 GCATCTTCTCTTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 355  
 Db 443 GCATCTTCTCTTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 384  
 QY 356 TGTGCGATGCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 415  
 Db 383 TGTGCGATGCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 324  
 QY 416 GGACGAGAGGCTCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 475  
 Db 323 GGACGAGAGGCTCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 264  
 QY 476 GGCGAGTGGCGGAGCTGCGATGACGCTTACGCTTACGCTTACGCTTACGCTTACGCTT 535  
 Db 263 GGCGAGTGGCGGAGCTGCGATGACGCTTACGCTTACGCTTACGCTTACGCTTACGCTT 204  
 QY 536 TGACTGCTCC 546  
 Db 203 TGACTGCTCC 193

RESULT 10  
 BG387051  
 LOCUS  
 DEFINITION 60245749F1 NIH\_MGC\_15 Homo sapiens CDNA clone IMAGE:4582933 5',  
 mRNA sequence.  
 ACCESSION BG387051  
 VERSION BG387051.1 GI:13280497  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: c9apbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: NIH Intramural Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 plate: L1CM1306 row: a column: 14  
 High quality sequence stop: 679.

FEATURES  
 source  
 1.832  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4582933"  
 /tissue\_type="adenocarcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_15"





RESULT 14			
B0723254			
LOCUS	B0723254	1093 bp	mRNA
DEFINITION	AGNCOURT_8486770	Lupsk1_sympathetic_trunk	linear
IMAGE:619636	5',	mrna sequence.	EST 16-JUL-2002
			Homo sapiens cDNA clone

1 (bases 1 to 1093)  
 NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA library Preparation: Life Technologies, Inc.  
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
 Plate: LNLN3604 row: k column: 23  
 High quality sequence stop: 437.

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/tissue_type="sympathetic trunk"
/dev stage="adult, 16 yr"
/lab host="DH10B"
/clone.lib="lupskel sympathetic trunk"
/note="vector: PCMV-8SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dt priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGACGCG-3' and
5'-GACGATGTTCAAGATCGCAGGCGCGCGCTT(15-3', size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupskel, M.D./Ph.D. (Baylor
College of Medicine); available through Life
technologies."

```

Query Match	85.0%;	Score 469,4;	DB 13;	length 1093;
Best Local Similarity	96.8%;	Pred. No. 1.8e-71;		
Matches 479: Conservative	0;	Mismatches 16;	Indels 0;	Gaps 0;

QY	44	TCACAGCCTCCCTGTGCAGCGCGCATGTGCGGGGACATCCGGGGGGCCCACTTCCAGAGCTTCC	103
Db	1	TCACAGCCTCCCTGTGCAGCGCGCATGTGCGGGGACATCCGGGGGGCCCACTTCCAGAGCTTCC	60
QY	104	AGAGAGCGCGGGGCGTGGGGGCTGGCGGGGACACTTCCGGCGCTTCTCTGTCTTGCGGCTTGC	163
Db	61	AGAGAGCGCGGGGCGTGGGGGCTGGCGGGGACACTTCCGGCGCTTCTCTGTCTTGCGGCTTGC	120
QY	164	AGGACCTGTACAGCATCTGTGCAGCGCGACCGCGCGACGCGTGGCCCATGTCAACTCA	223
Db	121	AGGACCTGTACAGCATCTGTGCAGCGCGACCGCGCGACGCGTGGCCCATGTCAACTCA	180
QY	224	AGGACGAGCTCTGTATCCAGCTGGGAGGCTGTCTCAGGCTCTGAGAGTCCGCTGA	283
Db	181	AGGACGAGCTGTATCCAGCTGGGAGGCTGTCTCAGGCTCTGAGAGTCCGCTGA	240
QY	284	AGCCCGGGGCACGATTTCTCTTTGACGGAGGAGCGTCTGAGGCCACCCCACTTGGC	343
Db	241	AGCCCGGGGCACGATTTCTCTTTGACGGAGGAGCGTCTGAGGCCACCCCACTTGGC	300
QY	344	CCGAGAGAGCGGTGTGCTGACCTGCACCCGACGGGCGAGGCTGACCGAGACTACT	403
Db	301	CCGAGAGAGCGGTGTGCTGACCTGCACCCGAGCGGAGGCTGACCGAGACTACT	360
QY	404	GTCGAGACGTGGCGGACGGAAGCTCCTCTGCGCAAGGCGCAAGGCTCTCTGTGCTGGGGGG	463
Db	361	GTCGAGACGTGGCGGAGCGGAGGCTCCTCTGCGCAAGGCGCGAGGCTCTCTGTGCTGGGGGG	420
QY	464	GCAGGCTCTGTGGGCGAAGTGTGCGGAACTTGCACATGAGGCTCTCATTTG	523
Db	421	GCAGGCTCTGTGGGCGAAGAGCGCGCAAGTGTGCTCATGACCGGTGACCTCTGGTGGCTAG	480
QY	524	AGAGCAGCTTCACTA	538
Db	481	AGAGCAGCTTCCCA	495

REFERENCE 1 (bases 1 to 664)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
INSTRUMENT Illumina

FEATURES  
 source  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 The following repetitive elements were found in this cDNA  
 sequence: 1-35, >AT richLow\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 FOLTA=yes  
 Location/Qualifiers  
 1..664  
 /organism="Homo sapiens"

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/db_xref="taxon:9606"  
/clone="UT-H-FEI-bea-m-09-0-UT"  
/tissue_type="Cell lines"  
/dev_stage="Adult"  
/lab_host="DH10B (Life Technologies)"  
/clone_1ib="NCI CGAP FE1"  
/note="Organ: Chondrosarcoma; Vector: pT73-Pac  
(pharmacia) with a modified polylinker; Site 1: EcoR I;  
Site 2: Not I; NCI CGAP FE1 is a normalized cDNA library  
derived from a pool of mRNA obtained from 3 cell lines  
from grade II chondrosarcoma tissues. The library was  
constructed according to Bonaldi, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT73-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
(DT)18 tail. The sequence tag for this library is  
CGCTACGAGC. The cell lines were provided by Dr James  
Martin from the University of Iowa.  
TAG TISSUE=Human grade 2 chondrosarcoma cell line pool  
TAG LIB=UT-H-FEI  
TAG_SEQ=CGCTACGAGC"
```

## ORIGIN

```
Query Match      83.0%; Score 453; DB 13; Length 664;  
Best Local Similarity 99.8%; Pred. No. 1,1e-68;  
Matches 453; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 93 CCAGTCTTCCAGCAGCGCGGCGCTGTGGGCGGCGACCTTCGCGCTTCTGTC 152  
DB 664 CCAGTCTTCCAGCAGCGCGGCGCTGTGGGCGGCGACCTTCGCGCTTCTGTC 605  
QY 153 CTGGGCGCTGCGAGGACCTGACAGATGTCGCGCGCCGACCGCGGACCGTGGCAT 212  
DB 604 CTGGGCGCTGCGAGGACCTGACAGATGTCGCGCGCCGACCGCGGACCGTGGCAT 545  
QY 213 CGTCAACTCAAGGACAGGCTGTTCCTCCAGCTGGAGGCTGTGTTCTCAGGCTGTA 272  
DB 544 CGTCAACTCAAGGACAGGCTGTTCCTCCAGCTGGAGGCTGTGTTCTCAGGCTGTA 485  
QY 273 GGGTCCGCTGAAGCGCGGCGCGCATTTCTCTTTGACGCGAAGGACGTCCTGAGCA 332  
DB 484 GGGTCCGCTGAAGCGCGGCGCGCATTTCTCTTTGACGCGAAGGACGTCCTGAGCA 425  
QY 484 GGGTCCGCTGAAGCGCGGCGCGCATTTCTCTTTGACGCGAAGGACGTCCTGAGCA 425  
DB 333 CCCCACTGGGCCCGAGAGAGCGTGTGSCATGTGCTGGAACCCCAACGGGCGAGGCTGAC 392  
DB 424 CCCCACTGGGCCCGAGAGAGCGTGTGSCATGTGCTGGAACCCCAACGGGCGAGGCTGAC 365  
QY 393 CGAGAGCTACTGTGAGACGTGGCGGACGAGGCTCCCTGGGCGACGGGCGAGGCTCTTC 452  
DB 364 CGAGAGCTACTGTGAGACGTGGCGGACGAGGCTCCCTGGGCGACGGGCGAGGCTCTTC 305  
QY 453 GGTGTGGGGGGCGAGGCTCTTGGGGCGAGGTGCGGAGCTGCCATCAGCCCTACATCGT 512  
DB 304 GGTGTGGGGGGCGAGGCTCTTGGGGCGAGGTGCGGAGCTGCCATCAGCCCTACATCGT 245  
QY 513 GCTTGCATTGAGACAGCTTCATGACTGCTCC 546  
DB 244 GCTTGCATTGAGACAGCTTCATGACTGCTCC 211
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Job time : 2457 secs

Sheet

(Blank)



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 19:29:47 ; Search time 355 Seconds

(without alignments)  
7738.624 Million cell updates/sec

Title: US-10-042-347-4

Sequence: 1 cacagccacgcgactcca.....acagctcatgactgcctcc 546

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PTC\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PTCUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	546	100.0	546	US-10-042-347-4	Sequence 4, Appl1
2	546	100.0	549	US-10-135-872B-10	Sequence 10, Appl1
3	546	100.0	549	US-10-131-241-53	Sequence 53, Appl1
4	546	100.0	549	US-10-292-418-3	Sequence 3, Appl1
5	546	100.0	552	US-09-873-676-30	Sequence 30, Appl1
6	546	100.0	552	US-09-878-531-2	Sequence 2, Appl1
7	546	100.0	552	US-10-607-501-1	Sequence 1, Appl1
8	546	100.0	555	US-10-449-609-3	Sequence 3, Appl1
9	546	100.0	627	US-09-373-938-4	Sequence 4, Appl1
10	546	100.0	1158	US-10-449-609-5	Sequence 3, Appl1
11	546	100.0	3394	US-09-880-107-2178	Sequence 2178, Appl1
12	546	100.0	4551	US-10-060-036-144	Sequence 144, Appl1
13	546	100.0	4875	US-10-264-049-835	Sequence 835, Appl1
14	545	99.8	551	US-10-080-797-2	Sequence 2, Appl1

15	542.8	99.4	641	US-10-432-364-4	Sequence 4, Appl1
16	538	98.5	555	US-10-210-172-161	Sequence 161, Appl1
17	534	97.8	534	US-10-042-347-6	Sequence 6, Appl1
18	534	97.8	534	US-10-131-241-59	Sequence 59, Appl1
19	493.6	90.4	540	US-10-131-241-48	Sequence 48, Appl1
20	419.6	76.8	552	US-10-131-241-50	Sequence 50, Appl1
21	419.6	76.8	552	US-10-292-418-34	Sequence 34, Appl1
22	418	76.6	555	US-09-938-391-3	Sequence 3, Appl1
23	418	76.6	829	US-09-938-391-1	Sequence 1, Appl1
24	416.4	76.3	482	US-10-210-172-163	Sequence 163, Appl1
25	405.6	74.3	480	US-10-210-172-165	Sequence 165, Appl1
26	381.2	69.8	558	US-09-775-125-3	Sequence 3, Appl1
27	381.2	69.8	558	US-09-775-125-3	Sequence 3, Appl1
28	381.2	69.8	555	US-10-036-869-37	Sequence 12, Appl1
29	381.2	69.8	573	US-09-998-831-12	Sequence 12, Appl1
30	381.2	69.8	573	US-10-373-561-12	Sequence 12, Appl1
31	379.6	69.5	552	US-10-292-418-17	Sequence 17, Appl1
32	379.6	69.5	624	US-09-373-938-1	Sequence 1, Appl1
33	379.6	69.5	624	US-10-080-797-4	Sequence 4, Appl1
34	379.6	69.5	624	US-10-422-934-70	Sequence 70, Appl1
35	316.8	58.0	632	US-10-131-241-51	Sequence 51, Appl1
36	301.8	55.3	306	US-10-430-503-37	Sequence 37, Appl1
37	240	44.0	574	US-10-060-036-64	Sequence 64, Appl1
38	193.4	35.4	4077	US-10-087-192-1454	Sequence 1454, Appl1
39	176.8	32.4	5204	US-09-971-392-159	Sequence 159, Appl1
40	176.8	32.4	5222	US-10-133-937-67	Sequence 67, Appl1
41	176.8	32.4	5222	US-10-159-563-67	Sequence 67, Appl1
42	134.8	24.7	6048	US-10-433-793-32	Sequence 32, Appl1
43	123	22.5	900	US-10-131-241-45	Sequence 45, Appl1
44	111.2	20.4	6048	US-10-433-793-31	Sequence 31, Appl1
45	110.4	20.2	338	US-10-469-285-423	Sequence 423, Appl1

## ALIGNMENTS

```

RESULT 1
US-10-042-347-4
; Sequence 4, Application US/10042347
; Publication No. US20030114370A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael S.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide Fragments
; FILE REFERENCE: 05213-0880 (43170-299874)
; CURRENT APPLICATION NUMBER: US/10/042,347
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 09/315,689
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 60/106,343
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 09/154,302
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: US 08/740,168
; PRIOR FILING DATE: 1996-10-22
; PRIOR APPLICATION NUMBER: US 60/005,835
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: US 60/023,070
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: US 60/026,263
; PRIOR FILING DATE: 1996-09-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-042-347-4
Query Match 100.0%; Score 546; DB 15; Length 546;
Best Local Similarity 100.0%; Pred. No. 1.9e-132;
Matches 546; Conservative 0; Mismatches 0; Gaps 0;

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QY 1 CACAGCCACCGGCACTTCCAGCCGGTGTCTCACTTGTGCTTCAACAGCCCTCTGTCA 60  
 DB 1 CACAGCCACCGGCACTTCCAGCCGGTGTCTCACTTGTGCTTCAACAGCCCTCTGTCA 60  
 QY 61 GGGGGGATGGGGGGGATCCGGGGGGGCGAGCTTCAGTGGCTTCAGAGGGGGGGGG 120  
 DB 61 GGGGGGATGGGGGGGATCCGGGGGGGCGAGCTTCAGTGGCTTCAGAGGGGGGGGG 120  
 QY 121 GGGCTGGGGGCACTTCCAGCCCTTCTGTCTGTGGCTTGGCAAGACCTTGTCAAGATC 180  
 DB 121 GGGCTGGGGGCACTTCCAGCCCTTCTGTCTGTGGCTTGGCAAGACCTTGTCAAGATC 180  
 QY 181 GTGGCGCTGTCCCAAGCGCGAGCGTGTCCCATGTCAACTCAAGAGAGAGGTGTGTT 240  
 DB 181 GTGGCGCTGTCCCAAGCGCGAGCGTGTCCCATGTCAACTCAAGAGAGAGGTGTGTT 240  
 QY 241 CCGAGCTGGAGGCTGTCTCAGGCTCTGAGGGGTCCGCTGAAGCCCGGGGCAAGCATC 300  
 DB 241 CCGAGCTGGAGGCTGTCTCAGGCTCTGAGGGGTCCGCTGAAGCCCGGGGCAAGCATC 300  
 QY 301 TTCTCTTTGACGGCAAGACGTCCTGAGGACCCCACTGGCTCCCAAGAGCGTGTGG 360  
 DB 301 TTCTCTTTGACGGCAAGACGTCCTGAGGACCCCACTGGCTCCCAAGAGCGTGTGG 360  
 QY 361 CATGGCTGGACCCCAAGCGGGGCGAGGCTGACCGAGAGCTACTGTGAGAGGTGGCGAAG 420  
 DB 361 CATGGCTGGACCCCAAGCGGGGCGAGGCTGACCGAGAGCTACTGTGAGAGGTGGCGAAG 420  
 QY 421 GAGGCTCCCTGGGCGACGAGGCTCTGTGTGGTGGGGGCGAGGCTCTGTGGGGGAG 480  
 DB 421 GAGGCTCCCTGGGCGACGAGGCTCTGTGTGGTGGGGGCGAGGCTCTGTGGGGGAG 480  
 QY 481 AGTGCCGCGAGCTGTGCATACGCGCTTACATGTGTCTGTGATGAGAAAGCTTCAAGAT 540  
 DB 481 AGTGCCGCGAGCTGTGCATACGCGCTTACATGTGTCTGTGATGAGAAAGCTTCAAGAT 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546

## RESULT 2

US-10-135-872B-10  
 ; Sequence 10, Application US/10135872B  
 ; Publication No. US20040071659A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chang, Betty  
 ; APPLICANT: Wu, Wei Wei  
 ; APPLICANT: McArthur, James  
 ; APPLICANT: Patel, Sallil  
 ; APPLICANT: Joos, Karin  
 ; APPLICANT: Mendez, Michael  
 ; APPLICANT: Donahue, Brian  
 ; TITLE OF INVENTION: Viral-Mediated Delivery and In Vivo Expression of  
 ; TITLE OF INVENTION: Polynucleotides Encoding Anti-Angiogenic Proteins  
 ; FILE REFERENCE: 3802-009-27  
 ; CURRENT APPLICATION NUMBER: US/10/135, 872B  
 ; CURRENT FILING DATE: 2002-04-29  
 ; PRIOR APPLICATION NUMBER: US 60/287,673  
 ; PRIOR FILING DATE: 2001-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/370,634  
 ; PRIOR FILING DATE: 2002-04-05  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 549  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-135-872B-10

Query Match 100.0%; Score 546; DB 12; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-132;

Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CACAGCCACCGGCACTTCCAGCCGGTGTCTCACTTGTGCTTCAACAGCCCTCTGTCA 60  
 DB 1 CACAGCCACCGGCACTTCCAGCCGGTGTCTCACTTGTGCTTCAACAGCCCTCTGTCA 60  
 QY 61 GGGGGGATGGGGGGGATCCGGGGGGGCGAGCTTCAGTGGCTTCAGAGGGGGGGGG 120  
 DB 61 GGGGGGATGGGGGGGATCCGGGGGGGCGAGCTTCAGTGGCTTCAGAGGGGGGGGG 120  
 QY 121 GGGCTGGGGGCACTTCCAGCCCTTCTGTCTGTGGCTTGGCAAGACCTTGTCAAGATC 180  
 DB 121 GGGCTGGGGGCACTTCCAGCCCTTCTGTCTGTGGCTTGGCAAGACCTTGTCAAGATC 180  
 QY 181 GTGGCGCTGTCCCAAGCGCGAGCGTGTCCCATGTCAACTCAAGAGAGAGGTGTGTT 240  
 DB 181 GTGGCGCTGTCCCAAGCGCGAGCGTGTCCCATGTCAACTCAAGAGAGAGGTGTGTT 240  
 QY 241 CCGAGCTGGAGGCTGTCTCAGGCTCTGAGGGGTCCGCTGAAGCCCGGGGCAAGCATC 300  
 DB 241 CCGAGCTGGAGGCTGTCTCAGGCTCTGAGGGGTCCGCTGAAGCCCGGGGCAAGCATC 300  
 QY 301 TTCTCTTTGACGGCAAGACGTCCTGAGGACCCCACTGGCTCCCAAGAGCGTGTGG 360  
 DB 301 TTCTCTTTGACGGCAAGACGTCCTGAGGACCCCACTGGCTCCCAAGAGCGTGTGG 360  
 QY 361 CATGGCTGGACCCCAAGCGGGGCGAGGCTGACCGAGAGCTACTGTGAGAGGTGGCGAAG 420  
 DB 361 CATGGCTGGACCCCAAGCGGGGCGAGGCTGACCGAGAGCTACTGTGAGAGGTGGCGAAG 420  
 QY 421 GAGGCTCCCTGGGCGACGAGGCTCTGTGTGGTGGGGGCGAGGCTCTGTGGGGGAG 480  
 DB 421 GAGGCTCCCTGGGCGACGAGGCTCTGTGTGGTGGGGGCGAGGCTCTGTGGGGGAG 480  
 QY 481 AGTGCCGCGAGCTGTGCATACGCGCTTACATGTGTCTGTGATGAGAAAGCTTCAAGAT 540  
 DB 481 AGTGCCGCGAGCTGTGCATACGCGCTTACATGTGTCTGTGATGAGAAAGCTTCAAGAT 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546

## RESULT 3

US-10-131-241-53  
 ; Sequence 53, Application US/10131241  
 ; Publication No. US20030012792A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Holaday, John W.  
 ; APPLICANT: Fortier, Anne H.  
 ; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer  
 ; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers  
 ; FILE REFERENCE: 05213-0344 43170-271565  
 ; CURRENT APPLICATION NUMBER: US/10/131,241  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: US 09/413,049  
 ; PRIOR FILING DATE: 1999-10-06  
 ; PRIOR APPLICATION NUMBER: US 09/316,802  
 ; PRIOR FILING DATE: 1999-05-21  
 ; PRIOR APPLICATION NUMBER: US 60/086,586  
 ; PRIOR FILING DATE: 1998-05-22  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 53  
 ; LENGTH: 549  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-131-241-53

Query Match 100.0%; Score 546; DB 15; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-132;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match	100.0%;	Score 546;	DB 15;	Length 549;
Best Local Similarity	100.0%;	Pred. No. 1.9e-132;		
Matches 546;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

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Query Match      100.0%; Score 546; DB 9; length 552;
Best Local Similarity 100.0%; Pred. No. 1,9e-112;
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGAGCCAGCGGCACTTCCAGGCGGATCTCCACATGTTGGCGTCAACAGCCCTTGTCA 60
Db      1 CAGAGCCAGCGGCACTTCCAGGCGGATCTCCACATGTTGGCGTCAACAGCCCTTGTCA 60

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QY	181	GTGCGCCCTGCGCCACCGCGACCGCTGCCATGCTCAACTGAAGACAGAGCGCTGTT	240
Db	181	GTGCGCCGTCGACCGCGACCGCTGCCATGCTCAACTGAAGACAGAGCTGCTTT	240
QY	241	CCGAGCTGGAGAGCTGTGTCTCAGGCTCTGAGGGTTCGCGTAAACCCGGGGCACGATC	300
Db	241	CCGAGCTGGAGAGCTGTGTTCTCAGGCTCTGAGGGTTCGCGTAAACCCGGGGCACATC	300
QY	301	TTCTCCTTTGACGCGCAAGACGTCTTGAGGACCCCACTGCGCCCCGAAAGAGCTGTGG	360
Db	301	TTCTCCTTTGACGCGCAAGACGTCTTGAGGACCCCACTGCGCCCCGAAAGAGCTGTGG	360
QY	361	CATGCGTCGAGACCCCAAGCGGGCGAGGCTGACGAGAGCTACTGTGACGTGTGGCGACG	420
Db	361	CATGCGTCGAGACCCCAAGCGGGCGAGGCTGACGAGAGCTACTGTGACGTGTGGCGACG	420
QY	421	GAGGCTCCCTCGGCGACAGGCGCAAGGCTCTCGCTGCTGGGGGGCAGGCTCTTGGGGACG	480
Db	421	GAGGCTCCCTCGGCGACAGGCGCAAGGCTCTCGCTGCTGGGGGGCAGGCTCTTGGGGACG	480
QY	481	AGTGGCGGAGCTGCACTACAGGCTTACATGTGTCTTGATTTGAGAACAGCTTCACTGACT	540
Db	481	AGTGGCGGAGCTGCACTACAGGCTTACATGTGTCTTGATTTGAGAACAGCTTCACTGACT	540
QY	541	GGCTCC 546	
Db	541	GGCTCC 546	

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RESULT 7
US-10-607-501-1
; Sequence 1, Application US/10607501
; Publication No. US20040091465A1
; GENERAL INFORMATION:
; APPLICANT: Yim, Zachary
; TITLE OF INVENTION: Therapeutic Antiangiogenic Compositions and Methods
; FILE REFERENCE: 05213-0791 (43170-286879)
; CURRENT APPLICATION NUMBER: US/10/607,501
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US 60/391,630
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-501-1

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Query Match	100.0 %;	Score 546;	DB 17;	Length 552;
Best Local Similarity	100.0 %;	Pred. No. 1.9e-123;		
Matches 546;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	CACAGCCACCGGACCTTCCAGCCGGTGTCCACCTGGTGGCTCAACAGCCCTCTGTCA	60	
Db	1	CACAGCCACCGGACCTTCCAGCCGGTGTCCACCTGGTGGCTCAACAGCCCTCTGTCA	60	
QY	61	GGCGCATGGGGGACATCCGCGGGGCGACCTTCAAGTCTTCCAGCAGGCGCGGCTCGTG	120	
Db	61	GGCGCATGGGGGACATCCGCGGGGCGACCTTCAAGTCTTCCAGCAGGCGCGGCTCGTG	120	
QY	121	GGGCTGGCGGGGACCTTTCGCGCTCTTCTCTGTCTCTCGCGCTTCCAGAGCTCTTACAGCATC	180	
Db	121	GGGCTGGCGGGGACCTTTCGCGCTCTTCTCTGTCTCTCGCGCTTCCAGAGCTCTTACAGCATC	180	
QY	181	GTGGCGCTGTGCCAGCCGCGCAGCGCTGCCCATGTGTAACTCAAGAGCAAGAGCTGTGTTT	240	
Db	181	GTGGCGCTGTGCCAGCCGCGCAGCGCTGCCCATGTGTAACTCAAGAGCAAGAGCTGTGTTT	240	
QY	241	CCGAGCTGGGAGGCTCTGTTCTCAAGGCTCTAAGGCTCCGCTGAAGCCCGGGGACGCACTC	300	
Db	241	CCGAGCTGGGAGGCTCTGTTCTCAAGGCTCTAAGGCTCCGCTGAAGCCCGGGGACGCACTC	300	

QY 301 TTCTCTTTGACGCGAAGAGAGCTCTGAGGCAACCCCACTGGCCCCAGAAAGCGTGTGG 360  
 Db 301 TTCTCTTTGACGCGAAGAGAGCTCTGAGGCAACCCCACTGGCCCCAGAAAGCGTGTGG 360  
 QY 361 CATGGCTTGAAG 420  
 Db 361 CATGGCTTGAAG 420  
 QY 421 GAGGCTTCTCCGCGCCCAAG 480  
 Db 421 GAGGCTTCTCCGCGCCCAAG 480  
 QY 481 AGTCCGAG 540  
 Db 481 AGTCCGAG 540  
 QY 541 GCCTCC 546  
 Db 541 GCCTCC 546  
 RESULT 8  
 US-10-449-609-3  
 ; Sequence 3, Application US/10449609  
 ; Publication No. US20040127407A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHEN, MEN Y  
 ; TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR  
 ; FILE REFERENCE: 035879-0163  
 ; CURRENT APPLICATION NUMBER: US/10/449,609  
 ; PRIOR FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: 60/384,121  
 ; PRIOR FILING DATE: 2002-05-31  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 555  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-449-609-3

Query Match 100.0%; Score 546; DB 17; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-132;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCCAGCCGAGTCTCACTGAGTGGGCTCAAGCCGCCCTGTCA 60  
 Db 4 CACAGCCACCGGCACTTCCAGCCGAGTCTCACTGAGTGGGCTCAAGCCGCCCTGTCA 63  
 QY 61 GCGGCAATGCGGCGCATCCGCGGCGGCGGACTTCCAGTGTCTTCCAGCAGGCGGCGCGT 120  
 Db 64 GCGGCAATGCGGCGCATCCGCGGCGGCGGACTTCCAGTGTCTTCCAGCAGGCGGCGCGT 123  
 QY 121 GGGCTGGGCGGCACTTCCGCGGCTTCTGCTCTGCGCCCTGCGAGAGACTTGAACGATC 180  
 Db 124 GGGCTGGGCGGCACTTCCGCGGCTTCTGCTCTGCGCCCTGCGAGAGACTTGAACGATC 183  
 QY 181 GTGCGCGTGCAGACCGGCGAGCCGTCGCCATGTCAACTCAAGAGACGAGTGTGTT 240  
 Db 184 GTGCGCGTGCAGACCGGCGAGCCGTCGCCATGTCAACTCAAGAGACGAGTGTGTT 243  
 QY 241 CCGAGCTGGAGGCTGTGTTCTGAGGCTTGAAGGTCGCTGAAGCCCGGCGGCAAGATC 300  
 Db 244 CCGAGCTGGAGGCTGTGTTCTGAGGCTTGAAGGTCGCTGAAGCCCGGCGGCAAGATC 303  
 QY 301 TTCTCTTTGACGCGAAG 360  
 Db 304 TTCTCTTTGACGCGAAG 363  
 QY 361 CATGGCTTGAAG 420

Db 364 CATGGCTTGAAG 423  
 QY 421 GAGGCTTCTCCGCGCCCAAG 480  
 Db 424 GAGGCTTCTCCGCGCCCAAG 483  
 QY 481 AGTCCGAG 540  
 Db 484 AGTCCGAG 543  
 QY 541 GCCTCC 546  
 Db 544 GCCTCC 549  
 RESULT 9  
 US-09-373-938-4  
 ; Sequence 4, Application US/09373938  
 ; Publication No. US20020115202A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hallenbeck, Paul  
 ; APPLICANT: Chen, Cheayun Theresa  
 ; TITLE OF INVENTION: ADENOVIRAL VECTORS INCLUDING DNA SEQUENCES ENCODING ANGIOGENIC INHIBITORS  
 ; FILE REFERENCE: 4-308992P1  
 ; CURRENT APPLICATION NUMBER: US/09/373,938  
 ; CURRENT FILING DATE: 1999-08-13  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 627  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(627)  
 ; OTHER INFORMATION:  
 US-09-373-938-4

Query Match 100.0%; Score 546; DB 13; Length 627;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-132;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCCAGCCGAGTCTCACTGAGTGGGCTCAAGCCGCCCTGTCA 60  
 Db 76 CACAGCCACCGGCACTTCCAGCCGAGTCTCACTGAGTGGGCTCAAGCCGCCCTGTCA 135  
 QY 61 GCGGCAATGCGGCGCATCCGCGGCGGCGGACTTCCAGTGTCTTCCAGCAGGCGGCGCGT 120  
 Db 136 GCGGCAATGCGGCGCATCCGCGGCGGCGGACTTCCAGTGTCTTCCAGCAGGCGGCGCGT 195  
 QY 121 GGGCTGGGCGGCACTTCCGCGGCTTCTGCTCTGCGCCCTGCGAGAGACTTGAACGATC 180  
 Db 196 GGGCTGGGCGGCACTTCCGCGGCTTCTGCTCTGCGCCCTGCGAGAGACTTGAACGATC 255  
 QY 181 GTGCGCGTGCAGACCGGCGAGCCGTCGCCATGTCAACTCAAGAGACGAGTGTGTT 240  
 Db 256 GTGCGCGTGCAGACCGGCGAGCCGTCGCCATGTCAACTCAAGAGACGAGTGTGTT 315  
 QY 241 CCGAGCTGGAGGCTGTGTTCTGAGGCTTGAAGGTCGCTGAAGCCCGGCGGCAAGATC 300  
 Db 316 CCGAGCTGGAGGCTGTGTTCTGAGGCTTGAAGGTCGCTGAAGCCCGGCGGCAAGATC 375  
 QY 301 TTCTCTTTGACGCGAAG 360  
 Db 376 TTCTCTTTGACGCGAAG 435  
 QY 361 CATGGCTTGAAG 420  
 Db 436 CATGGCTTGAAG 495  
 QY 421 GAGGCTTCTCCGCGCCCAAG 480  
 Db 496 GAGGCTTCTCCGCGCCCAAG 555

QY 481 AGTCCGCGAGCTGCATCCAGCTTACATGCTCTTCTGATTTGAGAAAGCTTCACT 540  
| | | | |  
Db 556 AGTCCGCGAGCTGCATCCAGCTTACATGCTCTTCTGATTTGAGAAAGCTTCACT 615  
QY 541 GCCTCC 546  
| | | | |  
Db 616 GCCTCC 621

RESULT 10  
US-10-449-609-5  
; Sequence 5, Application US/10449609  
; Publication No. US20040127407A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, MEN Y  
; TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR  
; FILE REFERENCE: 035879-0163  
; CURRENT APPLICATION NUMBER: US/10/449,609  
; CURRENT FILING DATE: 2003-09-26  
; PRIORITY APPLICATION NUMBER: 60/384,121  
; PRIORITY FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1158  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: hPRL\_G129R-Endostatin Fusion nucleotide sequence  
US-10-449-609-5

Query Match 100.0%; Score 546; DB 17; Length 1158;  
Best Local Similarity 100.0%; Pred. No. 1.8e-132;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGAGCTTCCAGCGGCTCTCACTGCTTGGCTTGGCTTCAAGCCCTGTC 60  
Db 607 CACAGCCACCGGAGCTTCCAGCGGCTCTCACTGCTTGGCTTGGCTTCAAGCCCTGTC 666  
QY 61 GGGCGCATGCGGGGATCCGCGGGGCGAGCTTCCAGGCTTCCAGAGCGCGGGCGT 120  
Db 667 GGGCGCATGCGGGGATCCGCGGGGCGAGCTTCCAGGCTTCCAGAGCGCGGGCGT 726  
QY 121 GGGCGCGGGGACCTTCCGCGCTTCTGCTCTGCGGCTGAGAGGAGCTTCAAGCATC 180  
Db 727 GGGCGCGGGGACCTTCCGCGCTTCTGCTCTGCGGCTGAGAGGAGCTTCAAGCATC 786  
QY 181 GTGCGCTGTCGCGAGCCGCGAGCGCTGCTTCACTTCAAGGAGAGAGCTTGT 240  
Db 787 GTGCGCTGTCGCGAGCCGCGAGCGCTGCTTCACTTCAAGGAGAGAGCTTGT 846  
QY 241 CCGAGCTGAGAGGCTGCTTCTCAAGGCTGAGAGGCTGAGAGCGCGGGGAGCATC 300  
Db 847 CCGAGCTGAGAGGCTGCTTCTCAAGGCTGAGAGGCTGAGAGCGCGGGGAGCATC 906  
QY 301 TTCTCTTTGAGCGGAGAGCTTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
Db 907 TTCTCTTTGAGCGGAG 966  
QY 361 CATGCTGAG 420  
Db 967 CATGCTGAG 1026  
QY 421 GAGGCTCTCTGCGGAG 480  
Db 1027 GAGGCTCTCTGCGGAG 1086  
QY 481 AGTCCGCGAGCTGCATCCAGCTTACATGCTCTTCTGATTTGAGAAAGCTTCACT 540  
Db 1087 AGTCCGCGAGCTGCATCCAGCTTACATGCTCTTCTGATTTGAGAAAGCTTCACT 1146

QY 541 GCCTCC 546  
| | | | |  
Db 1147 GCCTCC 1152

RESULT 11  
US-09-880-107-2178  
; Sequence 2178, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Iwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIORITY APPLICATION NUMBER: US 60/211,379  
; PRIORITY FILING DATE: 2000-06-14  
; PRIORITY APPLICATION NUMBER: US 60/237,054  
; PRIORITY FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2178  
; LENGTH: 3394  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L22548  
US-09-880-107-2178

Query Match 100.0%; Score 546; DB 9; Length 3394;  
Best Local Similarity 100.0%; Pred. No. 1.6e-132;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGAGCTTCCAGCGGCTCTCACTGCTTGGCTTGGCTTCAAGCCCTGTC 60  
Db 1504 CACAGCCACCGGAGCTTCCAGCGGCTCTCACTGCTTGGCTTGGCTTCAAGCCCTGTC 1563  
QY 61 GGGCGCATGCGGGGATCCGCGGGGCGAGCTTCCAGGCTTCCAGAGCGCGGGCGT 120  
Db 1564 GGGCGCATGCGGGGATCCGCGGGGCGAGCTTCCAGGCTTCCAGAGCGCGGGCGT 1623  
QY 121 GGGCGCGGGGACCTTCCGCGCTTCTGCTCTGCGGCTGAGAGGAGCTTCAAGCATC 180  
Db 1624 GGGCGCGGGGACCTTCCGCGCTTCTGCTCTGCGGCTGAGAGGAGCTTCAAGCATC 1683  
QY 181 GTGCGCTGTCGCGAGCCGCGAGCGCTGCTTCACTTCAAGGAGAGAGCTTGT 240  
Db 1684 GTGCGCTGTCGCGAGCCGCGAGCGCTGCTTCACTTCAAGGAGAGAGCTTGT 1743  
QY 241 CCGAGCTGAGAGGCTGCTTCTCAAGGCTGAGAGGCTGAGAGCGCGGGGAGCATC 300  
Db 1744 CCGAGCTGAGAGGCTGCTTCTCAAGGCTGAGAGGCTGAGAGCGCGGGGAGCATC 1803  
QY 301 TTCTCTTTGAGCGGAGAGCTTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
Db 1804 TTCTCTTTGAGCGGAGAGAGCTTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1863  
QY 361 CATGCTGAG 420  
Db 1864 CATGCTGAG 1923  
QY 421 GAGGCTCTCTGCGGAG 480  
Db 1924 GAGGCTCTCTGCGGAG 1983  
QY 481 AGTCCGCGAGCTGCATCCAGCTTACATGCTCTTCTGATTTGAGAAAGCTTCACT 540  
Db 1984 AGTCCGCGAGCTGCATCCAGCTTACATGCTCTTCTGATTTGAGAAAGCTTCACT 2043

QY 541 GCCTCC 546  
Db 2044 GCCTCC 2049

RESULT 12

US-10-060-036-144  
; Sequence 144, Application US/10060036  
; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yugui  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.566  
; CURRENT APPLICATION NUMBER: US/10/060,036  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 144  
; LENGTH: 4551  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-036-144

Query Match 100.0%; Score 546; DB 15; Length 4551;  
Best Local Similarity 100.0%; Pred. No. 1.6e-132;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 60  
Db 4000 CACAGCCACCGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4059  
QY 61 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 120  
Db 4060 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4119  
QY 121 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 180  
Db 4120 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4179  
QY 181 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 240  
Db 4180 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4239  
QY 241 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 300  
Db 4240 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4299  
QY 301 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 360  
Db 4300 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4359  
QY 361 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 420  
Db 4360 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4419  
QY 421 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 480  
Db 4420 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4479  
QY 481 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 540  
Db 4480 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4539  
QY 541 GCCTCC 546  
Db 4540 GCCTCC 4545

RESULT 13

US-10-264-049-835  
; Sequence 835, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA133PI  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: Patent In Ver. 3.1  
; SEQ ID NO 835  
; LENGTH: 4875  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-264-049-835

Query Match 100.0%; Score 546; DB 16; Length 4875;  
Best Local Similarity 100.0%; Pred. No. 1.6e-132;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 60  
Db 2512 CACAGCCACCGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 2571  
QY 61 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 120  
Db 2572 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 2631  
QY 121 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 180  
Db 2632 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 2691  
QY 181 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 240  
Db 2692 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 2751  
QY 241 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 300  
Db 2752 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 2811  
QY 301 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 360  
Db 2812 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 4299  
QY 361 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 420  
Db 2872 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 2931  
QY 421 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 480  
Db 2932 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 2991  
QY 481 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 540  
Db 2992 GGGGCGATGCGGGGACCTTCCAGCCGGTCCACCTGATGCGCTCAACAGCCCTCTGCA 3051  
QY 541 GCCTCC 546  
Db 3052 GCCTCC 3057

RESULT 14

US-10-080-797-2  
; Sequence 2, Application US/10080797  
; Publication No. US20020181253A1  
; GENERAL INFORMATION:

```

1 APPLICANT: Camprochiaro, Peter A.
2 APPLICANT: Dixon, Katharine H.
3 APPLICANT: Brazzell, Romulus K.
4 TITLE OF INVENTION: METHOD FOR TREATING OCULAR
5 TITLE OF INVENTION: NEOVASCULARIZATION
6 FILE REFERENCE: 4-31881A
7 CURRENT APPLICATION NUMBER: US/10/080,797
8 CURRENT FILING DATE: 2002-02-21
9
10 NUMBER OF SEQ ID NOS: 21
11
12 SOFTWARE: FastSeq For Windows Version 4.0
13
14 SEQ ID NO 2
15
16 LENGTH: 551
17
18 TYPE: DNA
19
20 ORGANISM: Human
21
22 US-10-080-797-2

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Query Match	99.8%	Score 545;	DB 14;	Length 551;
Best Local Similarity	100.0%	Pred. No. 3.4e-132;		
Matches 545;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	2	ACAGCCACCGGCACTTCCACACCGGTGTCTCCACCTGTGTCCTGACCTGACAGCCCCCTGTGTAC	61
Db	1	ACAGCCACCGGCACTTCCACACCGGTGTCTCCACCTGTGTCCTGACAGCCCCCTGTGTAC	60
QY	62	GCGGCATTGCGGGGCAATCCGGGGCCGACTTCCTTCCAGCTTCCAGCAGGGCGGGGCGTGG	121
Db	61	GCGGCATTGCGGGGCAATCCGGGGCCGACTTCCTTCCAGCTTCCAGCAGGGCGGGGCGTGG	120
QY	122	GAGCTGCGGGGCACTTCCCGGGCTTCCTGATCTCCGGGCTCGGGCTCGAGGACCTGTACAGCATCG	181
Db	121	GAGCTGCGGGGCACTTCCCGGGCTTCCTGATCTCCGGGCTCGGGCTCGAGGACCTGTACAGCATCG	180
QY	182	TGCGCCGTCGCAACCGGCGAGCGGTGACCATGTCAACTTCAGACGACGACTGTCTTTC	241
Db	181	TGCGCCGTCGCAACCGGCGAGCGGTGACCATGTCAACTTCAGACGACGACTGTCTTTC	240
QY	242	CCAGCTGGAGGAGCTGTCTTCTCAAGGCTGTGAGGGTCCGCTGAAGCCCGGGGGCAAGCATCT	301
Db	241	CCAGCTGGAGGAGCTGTCTTCTCAAGGCTGTGAGGGTCCGCTGAAGCCCGGGGGCAAGCATCT	300
QY	302	TCTCTTTTGAACGCGAAGGAGTCTCTTAGGACACCCCACTGGGCCCAAGAGGTGTGGC	361
Db	301	TCTCTTTTGAACGCGAAGGAGTCTCTTAGGACACCCCACTGGGCCCAAGAGGTGTGGC	360
QY	362	ATTGCTGTGGACCCCAAGGGGAGGAGGCTTGAACCGAGAGACTACTGTGAGACTGTGGCGGACG	421
Db	361	ATTGCTGTGGACCCCAAGGGGAGGAGGCTTGAACCGAGAGACTACTGTGAGACTGTGGCGGACG	420
QY	422	AAGGCTCTCTGGGCAACGGGCGAGGCTCTCTGGCTGTGGGGGGGAGGCTCTTGGGGGACGA	481
Db	421	AAGGCTCTCTGGGCAACGGGCGAGGCTCTCTGGCTGTGGGGGGGAGGCTCTTGGGGGACGA	480
QY	482	GTGCGCGAGCTGCCATACAGCTTAATGTGTCTCTGCAATTGAGAACAGGTTTCATGACATG	541
Db	481	GTGCGCGAGCTGCCATACAGCTTAATGTGTCTCTGCAATTGAGAACAGGTTTCATGACATG	540
QY	542	CCTTC	546
Db	541	CCTTC	545

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RESULT 15
US-10-432-364--4
; Sequence 4, Application US/10432364
; Publication No. US20040091996A1
; GENERAL INFORMATION:
; APPLICANT: VINGENE BIOTECHNOLOGY LIMITED
; TITLE OF INVENTION: A VIRUS WHICH CAN EXPRESS TUMOR ANGIOSTATIN FACTOR WITH HIGH EFF
; TITLE OF INVENTION: SPECIFIC TUMOR CELLS AND THE USE OF IT
; FILE REFERENCE: jec010042pct
; CURRENT APPLICATION NUMBER: US/10/432,364
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 36

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: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 641
: TYPE: DNA
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: The nucleotide sequence of the recovered fragments from PCR amplification of the human endostatin gene after being digested with EcoRI and
: OTHER INFORMATION: inserted into vector pPluscript IK3(+) (ATCC, USA)
: US-10-432-364-4

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Query Match	99.4%	Score 542.8;	DB 17;	Length 641;
Best Local Similarity	99.6%;	Pred. No. 1.2e-131;		
Matches 544;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY	1	CAGAGCAGCCGAGACTTCCAGGCGGAGTGTCTCACTGGATTGGGCTCAACAGGCCCCCTTCA	60
Db	82	CACAGCCACCCGAGCTTCAAGCCGGATGTCTCAACTGTGGCTCAACAGGCCCTCTCA	141
QY	61	GAGCGGACATCGGAGGCATCGCGGAGCGGACCTTCAAGTCTTTCAGAGGCGCGGCGTGTG	120
Db	142	GCGCGGATATCGGGGGCATATCGCGGAGCGGACCTTCAAGTCTTTCAGAGGCGCGGCGTGTG	201
QY	121	GAGGTGAGCGGAGACCTTCCGCGCTTCTCTGTCTTGCGGCTCGAGGAGACCTGTACAGATC	180
Db	202	GAGGTGAGCGGAGACCTTCCGCGCTTCTCTGTCTTGCGGCTCGAGGAGACCTGTACAGATC	261
QY	181	GTCGGCGCGTGCGAAGCGCGAGCGTGCGCATGTCATCACTCAAGAGCAGGTGCTGTTT	240
Db	262	GTCGGCGCGTGCGAAGCGCGAGCGTGCGCATGTCATCACTCAAGAGCAGGTGCTGTTT	321
QY	241	CCGAGCTGGAGAGCTGTCTTCAGGCTCTGAGAGGTTCGCTGAAGCCCGGAGCACGATC	300
Db	322	CCGAGCTGGAGAGCTGTCTTCAGGCTCTGAGAGGTTCGCTGAAGCCCGGAGCACGATC	381
QY	301	TTCTCTTTGACGGGAAAGACGTCTTGAGGTACCCCACTGGCCCCAGAGAGCGTGTGG	360
Db	382	TTCTCTTTTAAAGGAGAGAGCGTCTTGAGGTACCCCACTGGCCCCAGAGAGCGTGTGG	441
QY	361	CATAGGCTCGGAGCCCCAGCGGAGCGAGCTGACGAGAGCTACTGTGACAGCTGTGCGGACG	420
Db	442	CATAGGCTCGGAGCCCCAGCGGAGCGAGCTGACGAGAGCTACTGTGAGAGGTGTGGCGAGCG	501
QY	421	GAGGCTCCCTCGGAGCACGAGGCTTCCTCGGTCTTGGGAGGCGAGGCTCTCGGGGAG	480
Db	502	GAGGCTCCCTCGGAGCACGAGGCTTCCTCGGTCTTGGGAGGCGAGGCTCTCGGGGAG	561
QY	481	AGTATCGCGAGCTGCTCATACGCTTACATGTGTCTGATTGAGGAACAAGCTTACATGACT	540
Db	562	AGTATCGCGAGCTGCTCATACGCTTACATGTGTCTGATTGAGGAACAAGCTTACATGACT	621
QY	541	GGCTCC	546
Db	622	GGCTCC	627

Search completed: September 15, 2004, 21:20:46  
Job time : 357 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:04:38 ; Search time 2353 Seconds

(without alignments)  
10057.500 Million cell updates/sec

Title: US-10-042-347-4

Perfect score: 546  
Sequence: 1 caccgcccgcgcactcca.....acagctcatgactgcctcc 546

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 21671516395 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hhg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pt:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vt:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_mu:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vt:\*  
30: em\_hhg\_hum:\*  
31: em\_hhg\_inv:\*  
32: em\_hhg\_other:\*  
33: em\_hhg\_mus:\*  
34: em\_hhg\_pin:\*  
35: em\_hhg\_rtd:\*  
36: em\_hhg\_mam:\*  
37: em\_hhg\_vrt:\*  
38: em\_sy:\*  
39: em\_hhg\_hum:\*  
40: em\_hhg\_mus:\*  
41: em\_hhg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546	100.0	546	6	AR193165 Sequence
2	546	100.0	549	6	BD240882 Expressio
3	546	100.0	549	6	AX100086 Sequence
4	546	100.0	552	6	BD266741 Proteins
5	546	100.0	552	6	AX395662 Sequence
6	546	100.0	552	6	AX473835 Sequence
7	546	100.0	552	6	BD081407 Fused pro
8	546	100.0	563	6	AR418652 Sequence
9	546	100.0	786	6	AF282883 Homo sapi
10	546	100.0	900	6	AX370851 Sequence
11	546	100.0	1388	9	AK130835 Homo sapi
12	546	100.0	2364	9	AK098216 Homo sapi
13	546	100.0	2376	6	AX816106 Sequence
14	546	100.0	2376	6	AX816108 Sequence
15	546	100.0	3394	6	151045 Sequence 4
16	546	100.0	3394	6	AX409531 Sequence
17	546	100.0	3394	6	AX409531 Sequence
18	546	100.0	5408	9	AF018082 Homo sapi
19	546	100.0	5929	9	AF018081 Homo sapi
20	544.4	99.7	564	9	AF416592 Homo sapi
21	544.4	99.7	2637	9	BC033715 Homo sapi
22	538	98.5	555	9	AF184060 Homo sapi
23	534	97.8	534	6	AR193166 Sequence
24	534	97.8	537	6	AX100092 Sequence
25	520	95.2	650	6	AX370853 Sequence
26	426.2	78.1	552	6	BD272245 Anticangi
27	419.6	76.8	552	6	BD240900 Expressio
28	418	76.6	555	6	AX396311 Sequence
29	418	76.6	555	6	BD188111 Method an
30	418	76.6	829	6	AX396329 Sequence
31	418	76.6	829	6	BD188110 Method an
32	381.2	69.8	552	10	AF257775 Mus muscu
33	381.2	69.8	555	6	BD102800 Process f
34	381.2	69.8	555	6	BD128313 Endostati
35	381.2	69.8	558	6	AR268609 Sequence
36	381.2	69.8	565	6	AR100642 Sequence
37	381.2	69.8	565	6	E34073 Carrier/DNA
38	381.2	69.8	573	6	BD271283 Compositi
39	381.2	69.8	573	6	AR183471 Sequence
40	381.2	69.8	573	6	AR183520 Sequence
41	381.2	69.8	573	6	AR217279 Sequence
42	381.2	69.8	573	6	AR282751 Sequence
43	381.2	69.8	573	6	AX042272 Sequence
44	381.2	69.8	573	6	AX490666 Sequence
45	381.2	69.8	620	6	AR431858 Sequence

# ALIGNMENTS

RESULT 1  
AR193165  
LOCUS AR193165 546 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 4 from patent US 6346510.  
ACCESSION AR193165  
VERSION AR193165.1 GI:20239130  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 546)  
AUTHORS O'Reilly M.S. and Folkman M. Judah.  
TITLE Therapeutic angiogenic endostatin compositions  
JOURNAL Patent: US 6346510-A 4 12-FEB-2002;  
FEATURES Location/Qualifiers

## source

1. 546  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 546;  
Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCGGATGCTCACTGTTGGCTCAACAGCCCTGTCA 60  
DB 1 CACAGCCACCGGACCTTCCAGCGGATGCTCACTGTTGGCTCAACAGCCCTGTCA 60  
QY 61 GGGCGCATGCGGGGCAATCCGCGGGCCGACTTTCAGTCTCCAGAGCGCGGGCGTGG 120  
DB 61 GGGCGCATGCGGGGCAATCCGCGGGCCGACTTTCAGTCTCCAGAGCGCGGGCGTGG 120  
QY 121 GGGCGCATGCGGGGCAATCCGCGGGCCGACTTTCAGTCTCCAGAGCGCGGGCGTGG 180  
DB 121 GGGCGCATGCGGGGCAATCCGCGGGCCGACTTTCAGTCTCCAGAGCGCGGGCGTGG 180  
QY 181 GTGCGCGGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
DB 181 GTGCGCGGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
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DB 301 TTCTCTTTGACGGGCAAGGAGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
QY 361 CATGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
DB 361 CATGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
QY 421 GAGGCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480  
DB 421 GAGGCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480  
QY 481 AGTGCAGGAGCTGCTCAACGCTCAATGCTCTGATTTGAGAAAGCTTCACTACT 540  
DB 481 AGTGCAGGAGCTGCTCAACGCTCAATGCTCTGATTTGAGAAAGCTTCACTACT 540  
QY 541 GCCTCC 546  
DB 541 GCCTCC 546

RESULT 2  
BD240882 549 bp DNA linear PAT 17-JUL-2003  
LOCUS Expression and export of angiogenesis inhibitors as immunofusins.  
DEFINITION BD240882  
ACCESSION BD240882.1 GI:33050652  
KEYWORDS UP 2002523036-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 549)  
AUTHORS Lo, K.W., Li, X. and Gillies, S.D.  
TITLE Expression and export of angiogenesis inhibitors as immunofusins  
JOURNAL Patent: JP 2002523036-A 2 30-JUL-2002;  
LEXIGEN PHARMACEUTICALS CORP  
OS Homo sapiens (human)  
PN UP 2002523036-A/2  
PD 30-JUL-2002  
PR 25-AUG-1999 JP 2000566305  
PI KIM MING LO, YUE LI, STEPHEN D GILLIES  
PC C12N15/09, A61K31/711, A61K38/00, A61K39/395, A61K48/00, A61P7/00,

## FEATURES

## source

1. 549  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 549;  
Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCGGATGCTCACTGTTGGCTCAACAGCCCTGTCA 60  
DB 1 CACAGCCACCGGACCTTCCAGCGGATGCTCACTGTTGGCTCAACAGCCCTGTCA 60  
QY 61 GGGCGCATGCGGGGCAATCCGCGGGCCGACTTTCAGTCTCCAGAGCGCGGGCGTGG 120  
DB 61 GGGCGCATGCGGGGCAATCCGCGGGCCGACTTTCAGTCTCCAGAGCGCGGGCGTGG 120  
QY 121 GGGCGCATGCGGGGCAATCCGCGGGCCGACTTTCAGTCTCCAGAGCGCGGGCGTGG 180  
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QY 181 GTGCGCGGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
DB 181 GTGCGCGGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
QY 241 CCGAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGCTCTGAGGCGGCGGCGGCGGCGG 300  
DB 241 CCGAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGCTCTGAGGCGGCGGCGGCGGCGG 300  
QY 301 TTCTCTTTGACGGGCAAGGAGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
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QY 361 CATGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
DB 361 CATGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
QY 421 GAGGCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480  
DB 421 GAGGCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480  
QY 481 AGTGCAGGAGCTGCTCAACGCTCAATGCTCTGATTTGAGAAAGCTTCACTACT 540  
DB 481 AGTGCAGGAGCTGCTCAACGCTCAATGCTCTGATTTGAGAAAGCTTCACTACT 540  
QY 541 GCCTCC 546  
DB 541 GCCTCC 546

RESULT 3  
AX100086 549 bp DNA linear PAT 02-APR-2001  
LOCUS Sequence 4 from Patent W00119989.  
DEFINITION AX100086  
ACCESSION AX100086  
KEYWORDS AX100086.1 GI:13539061  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1  
AUTHORS Liang, H., Sim, K.L., Chang-Murad, A., Zhou, X., Madsen, J.,  
Boerner, R.J., Betrejo, L.L., Mistry, F.R., Shepard, S.R. and

TITLE Schrimsher, J. L.  
Method of producing and purifying endostatin?m protein  
JOURNAL Patent: WO 011989-A 4 22-MAR-2001;  
Entremed, Inc. (US)

FEATURES  
Source Location/Qualifiers  
1..549  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 549;  
Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCGCTGCA 60  
DB 1 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCGCTGCA 60  
QY 61 GCGGCAATGCGGGGCAATCCGGGGGCGGCACTTCCAGTGTCTCCAGAGGCGGGCGGTG 120  
DB 61 GCGGCAATGCGGGGCAATCCGGGGGCGGCACTTCCAGTGTCTCCAGAGGCGGGCGGTG 120  
QY 121 GGGCTGCGGGGCACTTCCGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
DB 121 GGGCTGCGGGGCACTTCCGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
QY 181 GTGCGCGGTGCGGCAATCCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 GTGCGCGGTGCGGCAATCCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 241 CCCAGCTGGAGGCTCTGTTCTGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGG 300  
DB 241 CCCAGCTGGAGGCTCTGTTCTGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGG 300  
QY 301 TTCTCTTTGACGGGCAAGGAGTCTGAGGCAATCCGCGGCGGCTGCTGCTGCTGCTGCT 360  
DB 301 TTCTCTTTGACGGGCAAGGAGTCTGAGGCAATCCGCGGCGGCTGCTGCTGCTGCTGCT 360  
QY 361 CATGCTCGGACCCCAACCGGCGGAGGCTGAGGCAATCCGCGGCGGCTGCTGCTGCTGCT 420  
DB 361 CATGCTCGGACCCCAACCGGCGGAGGCTGAGGCAATCCGCGGCGGCTGCTGCTGCTGCT 420  
QY 421 GAGGCTCTCTGCGGCAAGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 421 GAGGCTCTCTGCGGCAAGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
QY 481 AGTGCGGAGCTGCGCATACGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
DB 481 AGTGCGGAGCTGCGCATACGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
QY 541 GCCTCC 546  
DB 541 GCCTCC 546

RESULT 4  
BD266741  
LOCUS BD266741 552 bp DNA linear PAT 17-JUN-2003  
DEFINITION Proteins that bind angiogenesis-inhibiting proteins, compositions  
ACCESSION BD266741  
VERSION BD266741.1 GI:33076509  
KEYWORDS JP 2002532068-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 552)  
AUTHORS Macdonald, N.J. and Sim, K.L.  
TITL Proteins that bind angiogenesis-inhibiting proteins, compositions  
and methods of use thereof  
JOURNAL Patent: JP 2002532068-A 2 02-OCT-2002;

COMMENT

ENTREMED INC  
OS Homo sapiens (human)  
PN JP 2002532068-A/2  
PD 02-OCT-2002  
PF 06-DEC-1999 JP 2000585271  
PR 04-DEC-1998 US 09/206059  
PI NICHOLAS J MACDONALD, KIM LEB SIM  
PC C12N15/09, A61K38/00, A61P9/00, A61P27/02, A61P29/00, A61P35/00, PC  
A61P43/00,  
PC C07K14/705, G01N33/15, G01N33/50, G01N33/53, G01N33/566//A61K35/76, PC  
A61K45/00,  
PC A61K48/00, C12N15/00, A61K37/02  
CC Proteins that bind angiogenesis-inhibiting proteins, CC  
compositions and  
methods of use thereof  
FH Key Location/Qualifiers  
FT source 1..552  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 552;  
Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCGCTGCA 60  
DB 1 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCGCTGCA 60  
QY 61 GCGGCAATGCGGGGCAATCCGGGGGCGGCACTTCCAGTGTCTCCAGAGGCGGGCGGTG 120  
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QY 121 GGGCTGCGGGGCACTTCCGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
DB 121 GGGCTGCGGGGCACTTCCGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
QY 181 GTGCGCGGTGCGGCAATCCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
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QY 241 CCCAGCTGGAGGCTCTGTTCTGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGG 300  
DB 241 CCCAGCTGGAGGCTCTGTTCTGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGG 300  
QY 301 TTCTCTTTGACGGGCAAGGAGTCTGAGGCAATCCGCGGCGGCTGCTGCTGCTGCTGCT 360  
DB 301 TTCTCTTTGACGGGCAAGGAGTCTGAGGCAATCCGCGGCGGCTGCTGCTGCTGCTGCT 360  
QY 361 CATGCTCGGACCCCAACCGGCGGAGGCTGAGGCAATCCGCGGCGGCTGCTGCTGCTGCT 420  
DB 361 CATGCTCGGACCCCAACCGGCGGAGGCTGAGGCAATCCGCGGCGGCTGCTGCTGCTGCT 420  
QY 421 GAGGCTCTCTGCGGCAAGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 421 GAGGCTCTCTGCGGCAAGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
QY 481 AGTGCGGAGCTGCGCATACGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
DB 481 AGTGCGGAGCTGCGCATACGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
QY 541 GCCTCC 546  
DB 541 GCCTCC 546

RESULT 5  
AX395662

LOCUS AX395662 552 bp DNA linear PAT 18-MAY-2002  
 DEFINITION Sequence 30 from Patent WO0193897.  
 ACCESSION AX395662  
 VERSION AX395662.1 GI:21066471  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1  
 AUTHORS Sim, K.L. and Macdonald, N.J.  
 TITLE Angiotensin and endostatin binding proteins and methods of use  
 JOURNAL Patent: WO 0193897-A 30 13-DEC-2001;  
 Entremed, Inc. (US)  
 FEATURES  
 source location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Query Match 100.0%; Score 546; DB 6; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCAGCCGGTGTCCACCTGGTGGCTCAACAGCCCTGTCA 60  
 Db 1 CACAGCCACCGGCACTTCAGCCGGTGTCCACCTGGTGGCTCAACAGCCCTGTCA 60  
 QY 61 GCGGCGATGCGGGGCAATCCGCGGGGCGAGCTTCAGAGTCTTCAGAGCGCGGGCGTG 120  
 Db 61 GCGGCGATGCGGGGCAATCCGCGGGGCGAGCTTCAGAGTCTTCAGAGCGCGGGCGTG 120  
 QY 121 GGGCTGGGCGGCACTTCGGGCTTCTGCTGCTGCGGCTTCAGAGCTTCAGAGCTTC 180  
 Db 121 GGGCTGGGCGGCACTTCGGGCTTCTGCTGCTGCGGCTTCAGAGCTTCAGAGCTTC 180  
 QY 181 GTGGCGCGTGGCCAGCGCGAGCGGCTGCGGCTTCAGAGCTTCAGAGCTTCAGAGCTTC 240  
 Db 181 GTGGCGCGTGGCCAGCGCGAGCGGCTGCGGCTTCAGAGCTTCAGAGCTTCAGAGCTTC 240  
 QY 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTCAGAGGCTTCAGAGGCTTCAGAGGCTTCAG 300  
 Db 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTCAGAGGCTTCAGAGGCTTCAGAGGCTTCAG 300  
 QY 301 TTCTCTTTGACGGCAAGAGCTCTGAGGAGACCCACCTGCGCCAGAGAGCGGTGG 360  
 Db 301 TTCTCTTTGACGGCAAGAGCTCTGAGGAGACCCACCTGCGCCAGAGAGCGGTGG 360  
 QY 361 CATGGCTGGAGCCCGCAACGGGGGCGAGGCTGACGAGGCTGAGAGCTGAGAGCTGAGAG 420  
 Db 361 CATGGCTGGAGCCCGCAACGGGGGCGAGGCTGAGAGGCTGAGAGCTGAGAGCTGAGAG 420  
 QY 421 GAGGCTCCCTCGGCGACGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 Db 421 GAGGCTCCCTCGGCGACGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 QY 481 AGTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 Db 481 AGTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 QY 541 GCCTCC 546  
 Db 541 GCCTCC 546

RESULT 6  
 LOCUS AX473835 552 bp DNA linear PAT 09-AUG-2002  
 DEFINITION Sequence 2 from Patent WO0230982.  
 ACCESSION AX473835  
 VERSION AX473835.1 GI:22208005  
 KEYWORDS

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1  
 AUTHORS Sim, K.L. and Liang, H.  
 TITLE Angiogenesis-inhibiting peptides and proteins and methods of use  
 JOURNAL Patent: WO 0230982-A 2 18-APR-2002;  
 Entremed, Inc. (US)  
 FEATURES  
 source location/Qualifiers  
 1..552  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Query Match 100.0%; Score 546; DB 6; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCAGCCGGTGTCCACCTGGTGGCTCAACAGCCCTGTCA 60  
 Db 1 CACAGCCACCGGCACTTCAGCCGGTGTCCACCTGGTGGCTCAACAGCCCTGTCA 60  
 QY 61 GCGGCGATGCGGGGCAATCCGCGGGGCGAGCTTCAGAGTCTTCAGAGCGCGGGCGTG 120  
 Db 61 GCGGCGATGCGGGGCAATCCGCGGGGCGAGCTTCAGAGTCTTCAGAGCGCGGGCGTG 120  
 QY 121 GGGCTGGGCGGCACTTCGGGCTTCTGCTGCTGCTGCGGCTTCAGAGCTTCAGAGCTTC 180  
 Db 121 GGGCTGGGCGGCACTTCGGGCTTCTGCTGCTGCTGCGGCTTCAGAGCTTCAGAGCTTC 180  
 QY 181 GTGGCGCGTGGCCAGCGCGAGCGGCTGCGGCTTCAGAGCTTCAGAGCTTCAGAGCTTC 240  
 Db 181 GTGGCGCGTGGCCAGCGCGAGCGGCTGCGGCTTCAGAGCTTCAGAGCTTCAGAGCTTC 240  
 QY 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTCAGAGGCTTCAGAGGCTTCAGAGGCTTCAG 300  
 Db 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTCAGAGGCTTCAGAGGCTTCAGAGGCTTCAG 300  
 QY 301 TTCTCTTTGACGGCAAGAGCTCTGAGGAGACCCACCTGCGCCAGAGAGCGGTGG 360  
 Db 301 TTCTCTTTGACGGCAAGAGCTCTGAGGAGACCCACCTGCGCCAGAGAGCGGTGG 360  
 QY 361 CATGGCTGGAGCCCGCAACGGGGGCGAGGCTGACGAGGCTGAGAGCTGAGAGCTGAGAG 420  
 Db 361 CATGGCTGGAGCCCGCAACGGGGGCGAGGCTGACGAGGCTGAGAGCTGAGAGCTGAGAG 420  
 QY 421 GAGGCTCCCTCGGCGACGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 Db 421 GAGGCTCCCTCGGCGACGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 QY 481 AGTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 Db 481 AGTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 QY 541 GCCTCC 546  
 Db 541 GCCTCC 546

RESULT 7  
 LOCUS BD081407 552 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Fused protein containing angiotensin component and utilization thereof in antitumor therapy.  
 ACCESSION BD081407  
 VERSION BD081407.1 GI:22627010  
 KEYWORDS JP 2001518304-A/50.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 552)  
 AUTHORS Bolanowski, M.A., Caparon, M.H., Caspersen, G.F., Gregory, S.A.,  
 TITLE Klein, B.K. and McKearn, J.P.  
 JOURNAL Fused protein containing angiostatin component and utilization  
 thereof in antitumor therapy  
 Patent: JP 2001518304-A 50 16-Oct-2001;  
 GD SEARLE AND CO  
 COMMENT OS Homo sapiens (human)  
 PN JP 2001518304-A/50  
 PD 16-Oct-2001  
 PF 30-SEP-1998 JP 2000513958  
 PR 01-OCT-1997 US 60/060609  
 PI MARK A BOLANOWSKI, MAIRE H CAPARON, GERALD F CASPERSON, SUSAN A  
 PI GREGORY, J.  
 PI BARBARA K KLEIN, JOHN P MCKEARN  
 PC C12N15/09,A61K38/00,A61K48/00,A61P9/10,A61P35/00,C07K14/52, PC  
 C07K14/56,  
 CC Fused protein containing angiostatin component and utilization

FEATURES  
 source Location/Qualifiers  
 FT 1..552 /organism="Homo sapiens (human)"  
 CC antitumor therapy  
 FH Key Location/Qualifiers  
 FT source 1..552 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Query Match 100.0%; Score 546; DB 6; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACAGCCACGCGCATCTTCAGCGCGGTGCTCCACCTGTTGGCTTCAACACCCCTCTGTCA 60  
 1 CACAGCCACGCGCATCTTCAGCGCGGTGCTCCACCTGTTGGCTTCAACACCCCTCTGTCA 60  
 61 GGGCGCATGCGGCGCATCTTCAGCGCGGTGCTCCACCTGTTGGCTTCAACACCCCTCTGT 120  
 61 GGGCGCATGCGGCGCATCTTCAGCGCGGTGCTCCACCTGTTGGCTTCAACACCCCTCTGT 120  
 121 GGGCTGGCGGACCTTCGCGGCTTCTGCTGCTGCGGCTGCAAGACCTGTACAGCATC 180  
 121 GGGCTGGCGGACCTTCGCGGCTTCTGCTGCTGCGGCTGCAAGACCTGTACAGCATC 180  
 181 GTGGCGCGTGGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 181 GTGGCGCGTGGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 181 GTGGCGCGTGGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 241 CCGAGCTGGAGAGCTCTGTTCTCAGGCTCTGAGGCTGCGGCTGAGAGCCCGGCGGCGAGTC 300  
 241 CCGAGCTGGAGAGCTCTGTTCTCAGGCTCTGAGGCTGCGGCTGAGAGCCCGGCGGCGAGTC 300  
 301 TTCTCTTTTGAAGCGAAGAGCTCTGAGGCTGCGGCTGAGAGCCCGGCGGCGAGTC 360  
 301 TTCTCTTTTGAAGCGAAGAGCTCTGAGGCTGCGGCTGAGAGCCCGGCGGCGAGTC 360  
 361 CATGGCTGGAGCCCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 361 CATGGCTGGAGCCCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 421 GAGGCTCCCTGGCGCAGGCGCGAGGCTCTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 480  
 421 GAGGCTCCCTGGCGCAGGCGCGAGGCTCTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 480  
 481 AGTGGCGGAGCTGCGCATCAGGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 481 AGTGGCGGAGCTGCGCATCAGGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 541 GCCTCC 546

DB 541 GCCTCC 546

RESULT 8  
 LOCUS AR431862 563 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 9 from patent US 6653098.  
 ACCESSION AR431862  
 VERSION AR431862.1 GI:40194022  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 563)  
 AUTHORS Violand, B.N. and Harding, E.I.  
 TITLE Method of producing mouse and human endostatin  
 JOURNAL Patent: US 6653098-A 9 25-NOV-2003;  
 FEATURES Location/Qualifiers  
 source 1..563 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 100.0%; Score 546; DB 6; Length 563;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACAGCCACCGGAGATTCAGCGGCTCTCCACTGTTGGCTTCAACACCCCTCTGTCA 60  
 1 CACAGCCACCGGAGATTCAGCGGCTCTCCACTGTTGGCTTCAACACCCCTCTGTCA 60  
 6 CACAGCCACCGGAGATTCAGCGGCTCTCCACTGTTGGCTTCAACACCCCTCTGTCA 65  
 61 GGGCGCATGCGGCGCATCTTCAGCGGCGGTGCTCCACCTGTTGGCTTCAACACCCCTCTGT 120  
 66 GGGCGCATGCGGCGCATCTTCAGCGGCGGTGCTCCACCTGTTGGCTTCAACACCCCTCTGT 125  
 121 GGGCTGGCGGACCTTCGCGGCTTCTGCTGCTGCGGCTGCAAGACCTGTACAGCATC 180  
 126 GGGCTGGCGGACCTTCGCGGCTTCTGCTGCTGCGGCTGCAAGACCTGTACAGCATC 185  
 181 GTGGCGCGTGGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 186 GTGGCGCGTGGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 245  
 241 CCGAGCTGGAGAGCTCTGTTCTCAGGCTCTGAGGCTGCGGCTGAGAGCCCGGCGGCGAGTC 300  
 246 CCGAGCTGGAGAGCTCTGTTCTCAGGCTCTGAGGCTGCGGCTGAGAGCCCGGCGGCGAGTC 305  
 301 TTCTCTTTTGAAGCGAAGAGCTCTGAGGCTGCGGCTGAGAGCCCGGCGGCGAGTC 360  
 306 TTCTCTTTTGAAGCGAAGAGCTCTGAGGCTGCGGCTGAGAGCCCGGCGGCGAGTC 365  
 361 CATGGCTGGAGCCCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 366 CATGGCTGGAGCCCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 425  
 421 GAGGCTCCCTGGCGCAGGCGCGAGGCTCTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 480  
 426 GAGGCTCCCTGGCGCAGGCGCGAGGCTCTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 485  
 481 AGTGGCGGAGCTGCGCATCAGGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 486 AGTGGCGGAGCTGCGCATCAGGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 545  
 541 GCCTCC 546  
 546 GCCTCC 551

RESULT 9  
 LOCUS AF282883 786 bp mRNA linear PRI 14-JUN-2002  
 DEFINITION Homo sapiens multi-functional protein MFP mRNA, complete cds.

ACCESSION AF282883  
 VERSION AF282883.1 GI:21425750  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 786)  
 AUTHORS Dou, D.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JUN-2000) R & D, Robinson Biotech Corp., 24634 Five Mile Road, Suite 24-26, Redford, MI 48239, USA  
 FEATURES  
 source  
 1..786  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 1..786  
 /note="antiangiogenic agent"  
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 /product="multi-functional protein MFP"  
 /protein\_id="AA05249.1"  
 /db\_xref="GI:21425751"  
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ORIGIN  
 Query Match 100.0%; Score 546; DB 9; Length 786;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACAGCCACCGGCACTTCCAGCGGTCTCCAGCTGTTGCTGAACGCCCCCTGTCA 60  
 235 CACAGCCACCGGCACTTCCAGCGGTCTCCAGCTGTTGCTGAACGCCCCCTGTCA 294  
 61 GGGGGATGCGGGGATCCCGGGGCGCACTTCCAGGCTTCCAGGCGGGGCGG 120  
 295 GGGGGATGCGGGGATCCCGGGGCGCACTTCCAGGCTTCCAGGCGGGGCGG 354  
 121 GGGGGATGCGGGGATCCCGGGGCGCACTTCCAGGCTTCCAGGCTTCCAGGCT 180  
 355 GGGGGATGCGGGGATCCCGGGGCGCACTTCCAGGCTTCCAGGCTTCCAGGCT 414  
 181 GTGCGCGGTGCGGACCGCGGACCGTCCATCTCACTCAAGGAGAGCTGTGTT 240  
 415 GTGCGCGGTGCGGACCGCGGACCGTCCATCTCACTCAAGGAGAGCTGTGTT 474  
 241 CCGAGCTGAGAGCTCTGTTCAGGCTTCAAGGCTCCGTAAGCCCGGGGCAAGCATC 300  
 475 CCGAGCTGAGAGCTCTGTTCAGGCTTCAAGGCTCCGTAAGCCCGGGGCAAGCATC 534  
 301 TTCTCTTTGACGGGCAAGAGCTCTGAGGAGACCCCACTGSCCCCAAGAGAGGTGTG 360  
 535 TTCTCTTTGACGGGCAAGAGCTCTGAGGAGACCCCACTGSCCCCAAGAGAGGTGTG 594  
 361 CATGCTCGGAGCCCAAGGCGCAGAGCTGACCGAGAGCTGAGAGAGCTGTGCGAG 420  
 595 CATGCTCGGAGCCCAAGGCGCAGAGCTGACCGAGAGCTGAGAGAGCTGTGCGAG 654  
 421 GAGGCTTCTCGGCGCAGGCGCAGGCTCTCGTGTGCGGGGCGAGGCTCTGTGCGAG 480  
 655 GAGGCTTCTCGGCGCAGGCGCAGGCTCTCGTGTGCGGGGCGAGGCTCTGTGCGAG 714  
 481 AGTGGCGGAGCTGCGATCAGGCTTACATGCTGTGATTTAGAGAGAGCTTATGACT 540  
 715 AGTGGCGGAGCTGCGATCAGGCTTACATGCTGTGATTTAGAGAGAGCTTATGACT 774  
 541 GCCTCC 546  
 775 GCCTCC 780

RESULT 10  
 AX370851  
 LOCUS AX370851 900 bp DNA linear PAT 01-MAR-2002  
 DEFINITION Sequence 12 from Patent WO0210372.  
 ACCESSION AX370851  
 VERSION AX370851.1 GI:19168980  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1  
 AUTHORS Chapman, P.W., de Luca, G. and Falcioia, L.  
 TITLE Method of producing functional protein domains  
 JOURNAL Patent: WO 0210372-A 12 07-FEB-2002;  
 Applied Research Systems ARS Holding S.A. (AN)  
 FEATURES  
 source  
 1..900  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="mRNA for m1gsp fused to COL18A1 exons 38-41 for pmd-HR#1"

ORIGIN  
 Query Match 100.0%; Score 546; DB 6; Length 900;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACAGCCACCGGCACTTCCAGCGGTCTCCAGCTGTTGCTGAACGCCCCCTGTCA 60  
 337 CACAGCCACCGGCACTTCCAGCGGTCTCCAGCTGTTGCTGAACGCCCCCTGTCA 396  
 61 GGGGGATGCGGGGATCCCGGGGCGCACTTCCAGGCTTCCAGGCGGGGCGG 120  
 397 GGGGGATGCGGGGATCCCGGGGCGCACTTCCAGGCTTCCAGGCGGGGCGG 456  
 121 GGGGGATGCGGGGATCCCGGGGCGCACTTCCAGGCTTCCAGGCTTCCAGGCT 180  
 457 GGGGGATGCGGGGATCCCGGGGCGCACTTCCAGGCTTCCAGGCTTCCAGGCT 516  
 181 GTGCGCGGTGCGGACCGCGGACCGTCCATCTCACTCAAGGAGAGCTGTGTT 240  
 517 GTGCGCGGTGCGGACCGCGGACCGTCCATCTCACTCAAGGAGAGCTGTGTT 576  
 241 CCGAGCTGAGAGCTCTGTTCAGGCTTCAAGGCTCCGTAAGCCCGGGGCAAGCATC 300  
 577 CCGAGCTGAGAGCTCTGTTCAGGCTTCAAGGCTCCGTAAGCCCGGGGCAAGCATC 636  
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 637 TTCTCTTTGACGGGCAAGAGCTCTGAGGAGACCCCACTGSCCCCAAGAGAGGTGTG 696  
 361 CATGCTCGGAGCCCAAGGCGCAGAGCTGACCGAGAGCTGAGAGAGCTGTGCGAG 420  
 697 CATGCTCGGAGCCCAAGGCGCAGAGCTGACCGAGAGCTGAGAGAGCTGTGCGAG 756  
 421 GAGGCTTCTCGGCGCAGGCGCAGGCTCTCGTGTGCGGGGCGAGGCTCTGTGCGAG 480  
 757 GAGGCTTCTCGGCGCAGGCGCAGGCTCTCGTGTGCGGGGCGAGGCTCTGTGCGAG 816  
 481 AGTGGCGGAGCTGCGATCAGGCTTACATGCTGTGATTTAGAGAGAGCTTATGACT 540  
 817 AGTGGCGGAGCTGCGATCAGGCTTACATGCTGTGATTTAGAGAGAGCTTATGACT 876  
 541 GCCTCC 546  
 877 GCCTCC 882

RESULT 11  
 AK130835

Db	1031	CATGGCTGCGAAGCCCAACGAGGCGTACGAGAGCTACTGTGAGACGTGGCGAGAC	1090
Qy	421	GAAGCTCCCTCGAGCACGAGGACGAGGCTCCCTCGCTGCTGAGGAGCGAGGCTTCGGGGCAG	480
Db	1091	GAGGCTCCCTCGAGCACGAGGACGAGGCTCCCTCGCTGCTGAGGAGCGAGGCTTCGGGGCAG	1150
Qy	481	AGTGCAGGAGCTCCATCAACGCTCACTGTCCTGTGATATGAGAAACACTTCATGACT	540
Db	1151	AGTGCAGGAGCTCCATCAACGCTCACTGTCCTGTGATATGAGAAACACTTCATGACT	1210
Qy	541	GCCTCC 546	
Db	1211	GCCTCC 1216	
RESULT 12			
RSR216			
LOCUS		2364 bp	mRNA linear PRI 15-JUL-2002
DEFINITION	AK098216		homo sapiens cDNA FLJ40897 f1s, clone UTRR02002964, highly similar
ACCESSION	AK098216		
VERSION	AK098216.1	GI:21758185	
KEYWORDS		oligo capping, f1s (full insert sequence).	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS		1	
		Osihma,A., Takahashi,Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Misaashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,D., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Magatsuma,M., Murakawa,K., Kanemori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahara,K., Masuno,Y., Nagai,K. and Isogai,T.	
TITLE		NEBD human cDNA sequencing project	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 2364)	
AUTHORS		Isogai,T. and Yamamoto,J.	
TITLE		Direct Submission	
JOURNAL		Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team) ; 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomise@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEBD human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) ; cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.	
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		/tissue_type="uterus"	
		/clone_idb="UTR02"	
		/note="cloning vector: pME18SFL3"	
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		Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1644	CACAGCACCGAGCTTCACAGCGAGTGTCCACCGTGGTGCCTCAACAGCCCGCTGTCA 1703	
Qy	61	GGCGGCAATGGCGAGGATCCGCGGAGGCGCACTTCACATGCTTCACAGAGCGCGGAGCGTG 120	

Db 1704 GAGCGCATGGGGGCAATCCGGGGCCGACTTTCAGTGTCTTCCAGAGAGGGCGGGCGGTG 1763  
 QY 121 GGGCTGGCGGGGCACTTTCGGGCGCTTCTGTCTCTGCGCCCTGGCAGAGACTGTGACAGATC 180  
 Db 1764 GGGCTGGCGGGGCACTTTCGGGCGCTTCTGTCTCTGCGCCCTGGCAGAGACTGTGACAGATC 1823  
 QY 181 GTGGCGCGGTCCGACCGGGCGAGCGGTCCATGTCATCAACTCAAGGAGCGAGCTGTGTT 240  
 Db 1824 GTGGCGGTCCGACCGGCGAGCGGTCCATGTCATCAACTCAAGGAGCGAGCTGTGTT 1883  
 QY 241 CCCAGCTGGAGGCTGTCTGTCTGAGGCTTGAAGGCTGCGTAAAGCCCGGGGACGATC 300  
 Db 1884 CCCAGCTGGAGGCTGTCTGTCTGAGGCTTGAAGGCTGCGTAAAGCCCGGGGACGATC 1943  
 QY 301 TTCTCTTTGACGGCAAGAGAGCTCTGAGGACCCCACTGGGCCCCGAAAGAGCTGTGG 360  
 Db 1944 TTCTCTTTGACGGCAAGAGAGCTCTGAGGACCCCACTGGGCCCCGAAAGAGCTGTGG 2003  
 QY 361 CATGGCTGGAGCCCAACCGGGCGAGGCTGACCGAGGCTACTGTGAGAGCTGTGGGAGG 420  
 Db 2004 CATGGCTGGAGCCCAACCGGGCGAGGCTGACCGAGGCTACTGTGAGAGCTGTGGGAGG 2063  
 QY 421 GAGGCTCCCTCGGCGACCGGGCCAGGCTCTGCTGTGCTGGGGGCGAGGCTCTGGGGGAG 480  
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 QY 481 AGTCCCGGAGCTGCGATCAAGCTCTGATGCTGTGATTTGAAACAGCTTCATGACT 540  
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 QY 541 GCCTCC 546  
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RESULT 13  
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 LOCUS AX816106 2376 bp DNA linear PAT 09-DEC-2003  
 DEFINITION Sequence 30 from Patent WO0306085.  
 ACCESSION AX816106  
 VERSION AX816106.1 GI:39646687  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 artificial sequences.

REFERENCE  
 1 Mertins, P., Celik, I., Kisker, O., Sleep, D., Hay, J. and Hauser, H. P.  
 Albumin-fused anti-angiogenesis peptides  
 Patent: WO 0306085-A 30 14-AUG-2003;  
 JOURNAL Aventis Behring GmbH (DE) ; Delta Biotechnology Limited (GB)  
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 Location/Qualifiers  
 /organism="synthetic construct"  
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 /db\_xref="taxon:32630"  
 /note="Description of Artificial Sequence: DNA sequence of the N-terminal endostatin-albumin fusion open reading frame"

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 8e-78;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCCGAGTCTCAACTGTGTCGCTCAAGAGCCCTCTGTCA 60  
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 Db 133 GGGCGCATGGGGGCACTTCCGGGGGCGGACCTTCCAGAGGCTTCCAGAGGGCGGGCGGTG 192  
 QY 121 GGGGTGGGGGCACTTCCGGGGGCGGACCTTCCAGAGGCTTCCAGAGGGCGGGCGGTG 180

Db 193 GGGCTGGCGGGGCACTTTCGGGCGCTTCTGTCTCTGCGCCCTGGCAGAGACTGTGACAGATC 252  
 QY 181 GTGGCGCGGTCCGACCGGGCGAGCGGTCCATGTCATCAACTCAAGGAGCGAGCTGTGTT 240  
 Db 253 GTGGCGCGGTCCGACCGGCGAGCGGTCCATGTCATCAACTCAAGGAGCGAGCTGTGTT 312  
 QY 241 CCCAGCTGGAGGCTGTCTGTCTGAGGCTTGAAGGCTGCGTAAAGCCCGGGGACGATC 300  
 Db 313 CCCAGCTGGAGGCTGTCTGTCTGAGGCTTGAAGGCTGCGTAAAGCCCGGGGACGATC 372  
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 Db 373 TTCTCTTTGACGGCAAGAGAGCTCTGAGGACCCCACTGGGCCCCGAAAGAGCTGTGG 432  
 QY 361 CATGGCTGGAGCCCAACCGGGCGAGGCTGACCGAGGCTACTGTGAGAGCTGTGGGAGG 420  
 Db 433 CATGGCTGGAGCCCAACCGGGCGAGGCTGACCGAGGCTACTGTGAGAGCTGTGGGAGG 492  
 QY 421 GAGGCTCCCTCGGCGACCGGGCCAGGCTCTGCTGTGCTGGGGGCGAGGCTCTGGGGGAG 480  
 Db 493 GAGGCTCCCTCGGCGACCGGGCCAGGCTCTGCTGTGCTGGGGGCGAGGCTCTGGGGGAG 552  
 QY 481 AGTCCCGGAGCTGCGATCAAGCTCTGATGCTGTGATTTGAAACAGCTTCATGACT 540  
 Db 553 AGTCCCGGAGCTGCGATCAAGCTCTGATGCTGTGATTTGAAACAGCTTCATGACT 612  
 QY 541 GCCTCC 546  
 Db 613 GCCTCC 618

RESULT 14  
 AX816108  
 LOCUS AX816108 2376 bp DNA linear PAT 09-DEC-2003  
 DEFINITION Sequence 32 from Patent WO0306085.  
 ACCESSION AX816108  
 VERSION AX816108.1 GI:39646688  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 artificial sequences.

REFERENCE  
 1 Mertins, P., Celik, I., Kisker, O., Sleep, D., Hay, J. and Hauser, H. P.  
 Albumin-fused anti-angiogenesis peptides  
 Patent: WO 0306085-A 32 14-AUG-2003;  
 JOURNAL Aventis Behring GmbH (DE) ; Delta Biotechnology Limited (GB)  
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 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Description of Artificial Sequence: DNA sequence of the C-terminal albumin-endostatin fusion open reading frame"

ORIGIN  
 Query Match 100.0%; Score 546; DB 6; Length 2376;  
 Best Local Similarity 100.0%; Pred. No. 8e-78;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCCGAGTCTCAACTGTGTCGCTCAAGAGCCCTCTGTCA 60  
 Db 1828 CACAGCCACCGGACCTTCCAGCCGAGTCTCAACTGTGTCGCTCAAGAGCCCTCTGTCA 1887  
 QY 61 GGGCGCATGGGGGCACTTCCGGGGGCGGACCTTCCAGAGGCTTCCAGAGGGCGGGCGGTG 120  
 Db 1888 GGGCGCATGGGGGCACTTCCGGGGGCGGACCTTCCAGAGGCTTCCAGAGGGCGGGCGGTG 1947  
 QY 121 GGGCTGGGGGCACTTCCGGGGGCGGACCTTCCAGAGGCTTCCAGAGGGCGGGCGGTG 180  
 Db 1948 GGGCTGGGGGCACTTCCGGGGGCGGACCTTCCAGAGGCTTCCAGAGGGCGGGCGGTG 2007





(8/11/19)  
Fench

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:00:58; Search time 335 Seconds

(without alignments)  
6923.929 Million cell updates/sec

Title: US-10-042-347-4  
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Searched: 3373863 segs, 212409041 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	546	100.0	546	3	AAA27004 Human end
2	546	100.0	549	2	AAX77719 Human ang
3	546	100.0	549	3	AAZ51291 Human ang
4	546	100.0	549	3	AAA29884 Human ang
5	546	100.0	549	5	AA800867 Human gen
6	546	100.0	549	7	ABA00774 Human end
7	546	100.0	552	2	AAA53375 SBQ ID 50
8	546	100.0	552	3	AAA68203 Human end
9	546	100.0	552	3	AAZ51291 Human ang
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23	546	100.0	552	5	AAZ51291 Human ang

24	546	100.0	4875	6	AB054955
25	546	100.0	5408	2	AAZ77720
26	545	99.8	551	6	AB081193
27	542.8	99.4	641	4	AAH79104
28	542.8	99.4	641	6	AAU55454
29	542.8	99.4	641	6	AB076079
30	542.8	99.4	641	6	AAU4000
31	538	98.5	555	9	AAZ40255
32	534	97.8	534	3	AAA27005
33	534	97.8	537	5	AAZ08868
34	532.6	97.5	6462	3	AAZ4014
35	520	95.2	650	6	ABZ03978
36	426.2	78.1	552	3	AAZ50398
37	419.6	76.8	552	3	AAZ51309
38	418	76.6	555	6	AAU46063
39	418	76.6	828	6	AAU46062
40	416.4	76.3	482	9	AAZ40257
41	405.6	74.3	480	9	AAZ40259
42	381.2	69.8	555	2	AAZ79949
43	381.2	69.8	555	2	AAZ84635
44	381.2	69.8	555	5	AAZ88290
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## ALIGNMENTS

AB054955 Human ova  
Aax77720 Human col  
Abg81193 Human end  
Aab79104 Human end  
Aa155454 Specific  
Abg76079 Anticancer  
Aa14000 Reproduct  
Ade40255 Human NOV  
Aa27005 Alternate  
Aa00868 Human gen  
Aa64014 Nucleotid  
ABZ03978 Synthetic  
AAZ50398 Human end  
AAZ51309 Canine an  
Aa146063 Canine en  
Aa146062 Canine pr  
Ade40257 Human NOV  
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Aax79949 Endostati  
Aax84635 Mouse end  
Aac88290 Murine en  
Aad18701 Mouse end

## RESULT 1

AAA27004 standard; DNA, 546 BP.

AAA27004;

11-AUG-2000 (first entry)

Human endostatin gene.

Human; endostatin cell proliferation inhibitor; collagen XVIII;  
angiogenesis inhibitor; anti-tumour; cytostatic; antiproliferative;  
vasotropic; dermatological; ophthalmological; vulnary;  
antitreticlosclerotic; antidiabetic; haemostatic; contriceptive;  
ocular angiogenic disease; atherosclerosis; scleroderma;  
myocardial angiogenesis; telangiectasia; angiodioma;  
wound granulation, ds.

Homo sapiens.

Key Location/Qualifiers  
1..546  
/\*tag= a  
/product= "Endostatin protein"

MO200026368-A2.

01-NOV-1999; 99WO-US025605.

30-OCT-1998; 98US-0106343P.

20-MAY-1999; 99US-00315689.

(CHIL-) CHILDRENS MEDICAL CENT.

O'Reilly MS, Folkman MJ;

WPI; 2000-365617/31.

P-PSDB; AAY94323.

Novel endostatin capable of inhibiting endothelial cell proliferation and

angiogenesis, useful for treating angiogenesis-dependent cancers and as

birth control agents.  
Claim 10; Page 39; 68pp; English.

XX The present sequence encodes an endostatin protein which is the carboxy  
CC terminal protein of human collagen XVIII. Recombinant mouse endostatin  
CC (20 mg/kg) was administered subcutaneously to mice implanted with Lewis  
CC lung carcinomas. There was tumour mass regression non-detectable levels  
CC after 12 days of therapy due to the angiogenesis inhibitory activity of  
CC endostatin. Thus the protein is useful for treatment of angiogenesis-  
CC dependent cancers. The polynucleotide and polypeptide sequences of this  
CC endostatin are useful for treating and diagnosis of tumours, ocular  
CC angiogenic diseases, Osler-Weber syndrome, myocardial angiogenesis,  
CC plaque neovascularisation, telangiectasia, haemophilic joints,  
CC angioblastoma and wound granulation, for treatment of diseases related to  
CC excessive or abnormal stimulation of endothelial cells e.g. intestinal  
CC adhesions, atherosclerosis, scleroderma. The protein may also be useful  
CC as a birth control agent by reducing or preventing uterine  
CC vascularisation. The gene for endostatin may be isolated from cells or  
CC tissue that express high levels of endostatin, eg. tumour cells, by  
CC generating cDNA from mRNA using reverse transcriptase and then amplifying  
CC the DNA sequence

XX Sequence 546 BP; 80 A; 196 C; 177 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 3; Length 546;  
Best Local Similarity 100.0%; Pred. No. 5.1e-102;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 CACAGCCACCGCGAATTCCAGCGGTGCTCCAGCTGTTGCGCTCAACAGCCCCCTGTCA 60  
DB 1 CACAGCCACCGCGAATTCCAGCGGTGCTCCAGCTGTTGCGCTCAACAGCCCCCTGTCA 60  
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DB 61 GGGGGGATGCGGGGATCCCGGGGCGGACCTTCAGAGCTCCACAGCGCGGGCGG 120  
YY 121 GGGCTGGGGGACCTTCGCGGCTTCTGCTGCTGCGGCTGAGAGACTGTACAGCATC 180  
DB 121 GGGCTGGGGGACCTTCGCGGCTTCTGCTGCTGCGGCTGAGAGACTGTACAGCATC 180  
YY 181 GTGGCGCGTGGCGGACCGGCGGAGCGGTGCTCACTCAAGAGAGAGCTGCTTT 240  
DB 181 GTGGCGCGTGGCGGACCGGCGGAGCGGTGCTCACTCAAGAGAGAGCTGCTTT 240  
YY 241 CCCAGCTGGAGGCTTCTTCTCAGAGCTGTAGAGGCTCGGTGAGAGCGGGGCGGATC 300  
DB 241 CCCAGCTGGAGGCTTCTTCTCAGAGCTGTAGAGGCTCGGTGAGAGCGGGGCGGATC 300  
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DB 301 TTCTCTTTGAGCGGAGAGAGCTGTAGAGGCTCGGTGAGAGCGGGGCGGATC 360  
YY 361 CATGGCTCGGACCGGAGCGGAGCTGTAGAGGCTCGGTGAGAGCGGGGCGGATC 420  
DB 361 CATGGCTCGGACCGGAGCGGAGCTGTAGAGGCTCGGTGAGAGCGGGGCGGATC 420  
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DB 421 GAGGCTCTCTCGGCGGAGCGGAGCTGTAGAGGCTCGGTGAGAGCGGGGCGGATC 480  
YY 481 AGTGGCGGAGCTGTAGAGGCTGTAGAGGCTGTAGAGGCTGTAGAGGCTGTAGAT 540  
DB 481 AGTGGCGGAGCTGTAGAGGCTGTAGAGGCTGTAGAGGCTGTAGAGGCTGTAGAT 540  
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DB 541 GCGTCC 546

RESULT 2  
AAK77719  
ID AAK77719 standard; DNA; 549 BP.  
XX  
AC AAK77719;  
XX

DT 10-AUG-1999 (first entry)

XX Human endostatin DNA coding region fragment.  
DE  
XX Plasmidogen; human; angiotensin; endostatin; gene therapy; vector;  
KW anti-angiogenic; attenuation; cytosolic; anti-diabetic; ophthalmology;  
KW tumour growth; solid tumour; diabetic retinopathy; retina; ss.

XX Homo sapiens.

PN MO9926480-A1.

XX 03-JUN-1999.

XX 20-NOV-1998; 98MO-US024950.

XX 20-NOV-1997; 97US-00975424.

XX (GENE-) GENETIX PHARM INC.

XX (MAST) MASSACHUSETTS INST TECHNOLOGY.

XX Leboulch P, Pawliuk RJ, Bachelot T;

XX WPI, 1999-357696/30.

XX P-PSDB; AAY08693.

XX Anti-angiogenic gene therapy vectors.

XX Disclosure; Page 74; 83pp; English.

CC This invention describes a novel viral gene therapy vector comprising a  
CC nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from  
CC human or murine angiotensin, human or murine endostatin and angiotensin-  
CC inhibiting fusions and fragments, where the viral vector is sufficiently  
CC attenuated for use in human gene therapy. The products of the invention  
CC have anti-angiogenic, cytosolic, anti-diabetic and ophthalmological  
CC activity. The vector is used in gene therapy for inhibiting tumour growth  
CC in humans harbouring a solid tumour. The vector expresses an anti-  
CC angiogenic polypeptide. An additional use comprises treatment of diabetic  
CC retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis  
CC in the vicinity of the retina. The vector is administered to cells ex  
CC vivo and then administered to the patient

SQ Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 2; Length 549;  
Best Local Similarity 100.0%; Pred. No. 5.1e-102;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 CACAGCCACCGCGAATTCCAGCGGTGCTCCAGCTGTTGCGCTCAACAGCCCCCTGTCA 60  
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DB 61 GGGGGGATGCGGGGATCCCGGGGCGGACCTTCAGAGCTCCACAGCGCGGGCGG 120  
YY 121 GGGCTGGGGGACCTTCGCGGCTTCTGCTGCTGCGGCTGAGAGACTGTACAGCATC 180  
DB 121 GGGCTGGGGGACCTTCGCGGCTTCTGCTGCTGCGGCTGAGAGACTGTACAGCATC 180  
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DB 241 CCCAGCTGGAGGCTTCTTCTCAGAGCTGTAGAGGCTGTAGAGGCTGTAGAGGCTGTAGAT 300  
YY 301 TTCTCTTTGAGCGGAGAGAGCTGTAGAGGCTGTAGAGGCTGTAGAGGCTGTAGAT 360  
DB 301 TTCTCTTTGAGCGGAGAGAGCTGTAGAGGCTGTAGAGGCTGTAGAGGCTGTAGAT 360

	CC	blood born tumours, tumor metastasis, benign tumours including
	CC	haemangiomas, acoustic neuromas, neurofibromas, trichomas and pyrogenic
	CC	granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases
	CC	e.g. diabetic retinopathy, rejection of prematurity, macular
	CC	dysplasia, corneal graft rejection, neovascular glaucoma, retrolental
	CC	fibropia, rubosis and Osler-Weber syndrome; myocardial angiogenesis,
	CC	angioblastoma, wound granulation, and excessive or abnormal stimulation of
	CC	endothelial cells, intestinal scars, keloid scars, sclerodermal and
	CC	hyperkeratotic scars, i.e. keloid scars. The DNA constructs may be used in
	CC	gene therapy. The present sequence is a cDNA encoding human endostatin
	CC	used in the construction of immunofusion containing human immunoglobulin
	CC	gamma (IgG) Fc fragment. Note: This sequence is stated in claim 12 as
	CC	being amino acid sequence of plasmidogen fragment, however, the rest of
	CC	the specification refers to this sequence as being nucleotide sequence of
	CC	human endostatin
	XX	
SQ	Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other;	
Query Match	100.0%; Score 546; DB 3; Length 549;	
Best Local Similarity	100.0%; Pied. No. 5.1e-102;	
Matches 546; Conservative 0;	Mismatches 0; Indels 0; Gaps 0	
QY	1 CACAGCACCGCGAATTTCACAGCGCGGTCCATCTTGCGTCAACAGCCCCCTGCACA	60
DB	1 CACAGCACCGCGAATTTCACAGCGCGGTCCATCTTGCGTCAACAGCCCCCTGCACA	60
QY	61 GCACGCAATGGCGGAGCATCCGCGGAGCCGACTTCACATGTTTCACAGCAGCGCGGCGT	120
DB	61 GCACGCAATGGCGGAGCATCCGCGGAGCCGACTTCACATGTTTCACAGCAGCGCGGCGT	120
QY	121 GAGCGTGGCGGAGCACTTTCGCGGCTTCTTCTGCTGCGGCTGCGAGCCTGTACAGCATC	180
DB	121 GAGCGTGGCGGAGCACTTTCGCGGCTTCTTCTGCTGCGGCTGCGAGCCTGTACAGCATC	180
QY	181 GTGCGCGTGGCGAGCCGCGAGCGTCCATGTAACCTCAGAAGCAGCGTGTGTTT	240
DB	181 GTGCGCGTGGCGAGCCGCGAGCGTCCATGTAACCTCAGAAGCAGCGTGTGTTT	240
QY	241 CCCAGCTGGGAGGCTCTGTTTCAGAGCTTGAAGGTTCCGCTGAAGGCCCGGAGCAGCATC	300
DB	241 CCCAGCTGGGAGGCTCTGTTTCAGAGCTTGAAGGTTCCGCTGAAGGCCCGGAGCAGCATC	300
QY	301 TTTCCTTTGAGGAGAGAGTCTCTGAGGACAACCACCTGCGCCAGAAAGCGTGTGG	360
DB	301 TTTCCTTTGAGGAGAGAGTCTCTGAGGACAACCACCTGCGCCAGAAAGCGTGTGG	360
QY	361 CATGCGTGGAGCCCAAAGGAGCGAGCTGACCGAAGCTACTGTGAGACGTTGCGGAGAG	420
DB	361 CATGCGTGGAGCCCAAAGGAGCGAGCTGACCGAAGCTACTGTGAGACGTTGCGGAGAG	420
QY	421 GAGGCTTCCTGGGCAAGGGGCAAGGCTCTCTGCTGCTGCGGAGGAGCGTCTTGGGAGAG	480
DB	421 GAGGCTTCCTGGGCAAGGGGCAAGGCTCTCTGCTGCTGCGGAGGAGCGTCTTGGGAGAG	480
QY	481 AGTGGCGAGAGCTTCCATCAGCGCTACATGATGATGATGATAAGAGAGTGTACAGT	540
DB	481 AGTGGCGAGAGCTTCCATCAGCGCTACATGATGATGATGATAAGAGAGTGTACAGT	540
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DB	541 GCGTCC 546	
RESULT 4		
ID	AAA29884	
CDNA	AAA29884 standard; cDNA, 549 BP.	
AC	AAA29884;	
DE	22-AUG-2000 (first entry)	

XX Human; angiogenesis inhibiting factor 1; IAF-1; tumour; antibody;  
 KW abnormal vessel disease; ss.  
 XX Homo sapiens.  
 XX CNI244536-A.  
 XX 16-FEB-2000.  
 XX 10-AUG-1998; 98CN-00117150.  
 XX 10-AUG-1998; 98CN-00117150.  
 XX (ONCO-) INST ONCOLOGY UNDER TUMOR HOSPITAL CHINE.  
 XX Yang Z, Guo W;  
 XX WPI; 2000-388168/34.  
 XX P-PSDB; AA90771.  
 XX Angiogenesis inhibiting factor 1 and its derivative useful for treating  
 PT tumors.  
 XX Example 1; Fig 5; 41pp; Chinese.  
 XX The present sequence encodes an angiogenesis inhibiting factor (1),  
 CC designated IAF-1. The present invention also describes: (1) preparation  
 CC of (1) and its derivative; (2) an IAF binding acceptor and its  
 CC preparation; and (3) an IAF antibody. (1) is useful for preparing new  
 CC biological preparations for effectively treating various tumours and  
 CC abnormal-vessel diseases. The IAF antibody is preferably a polyclonal  
 CC antibody, mosaic antibody, single stranded antibody and human originated  
 CC antibody  
 XX  
 SQ Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 546; DB 3; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-102; Mismatches 0; Gaps 0;  
 Matches 546; Conservative 0; Indels 0;  
 QY 1 CACAGCCACCGGACCTTCAGCCGCGTCCAGCTGGTCCGCTCAAGAGCCCTCTGTCA 60  
 DB 1 CACAGCCACCGGACCTTCAGCCGCGTCCAGCTGGTCCGCTCAAGAGCCCTCTGTCA 60  
 QY 61 GGGCGCATGCGGGGATCCGGGGGCGGACCTTCAGCTGGTCCGCTCAAGAGCCCTCTGT 120  
 DB 61 GGGCGCATGCGGGGATCCGGGGGCGGACCTTCAGCTGGTCCGCTCAAGAGCCCTCTGT 120  
 QY 121 GGGCGCATGCGGGGATCCGGGGGCGGACCTTCAGCTGGTCCGCTCAAGAGCCCTCTGT 180  
 DB 121 GGGCGCATGCGGGGATCCGGGGGCGGACCTTCAGCTGGTCCGCTCAAGAGCCCTCTGT 180  
 QY 181 GTGGCGGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 DB 181 GTGGCGGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 QY 241 CCGAGCTGGAGGCTCTGTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCT 300  
 DB 241 CCGAGCTGGAGGCTCTGTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCT 300  
 QY 301 TTCTCCCTTTAGCGGCAAGAGCTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCT 360  
 DB 301 TTCTCCCTTTAGCGGCAAGAGCTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCT 360  
 QY 361 CATGCTCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 DB 361 CATGCTCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 QY 421 GAGGCTCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480  
 DB 421 GAGGCTCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480

QY 481 AGTGGCGGAGCTCCATCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCT 540  
 DB 481 AGTGGCGGAGCTCCATCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCT 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546  
 RESULT 5  
 ID AAS00867  
 AC AAS00867 standard; DNA; 549 BP.  
 DT 04-JUL-2001 (first entry)  
 DE Human gene fragment encoding Endostatin(TM) protein.  
 XX Human; Endostatin(TM); angiogenesis mediated disease; solid tumours;  
 KW blood borne tumour; leukaemia; tumour metastasis; benign tumour;  
 KW haemangioma; acoustic neuroma; neurofibroma; trachoma; rubecosis;  
 KW pyogenic granuloma; rheumatoid arthritis; psoriasis; colon cancer;  
 KW ocular angiogenic disease; diabetic retinopathy; macular degeneration;  
 KW retinopathy of prematurity; macular corneal graft rejection;  
 KW neovascular glaucoma; retrolental fibroplasia; Osler-Weber Syndrome;  
 KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;  
 KW haemophilic joint; angiofibroma; wound granulation; ds.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1. 549  
 FT CDS  
 FT /tag= d  
 FT /product= "Endostatin(TM)"  
 FT /note= "None of the above CDSs have start or stop codons"  
 FT /partial  
 FT CDS  
 FT 1. 546  
 FT /tag= c  
 FT /product= "Endostatin(TM) C-terminus minus 1"  
 FT /note= "Variant produced during fermentation reaction of  
 Pichia pastoris harbouring an expression plasmid  
 containing the present sequence"  
 FT /partial  
 FT CDS  
 FT 1. 543  
 FT /tag= b  
 FT /product= "Endostatin(TM) C-terminus minus 2"  
 FT /note= "Variant produced during fermentation reaction of  
 Pichia pastoris harbouring an expression plasmid  
 containing the present sequence"  
 FT /partial  
 FT CDS  
 FT 1. 540  
 FT /tag= a  
 FT /product= "Endostatin(TM) C-terminus minus 3"  
 FT /note= "Variant produced during fermentation reaction of  
 Pichia pastoris harbouring an expression plasmid  
 containing the present sequence"  
 FT /partial  
 PN W0200119989-A2.  
 PD 22-MAR-2001.  
 PF 14-SEP-2000; 2000WO-US025166.  
 PR 14-SEP-1999; 99US-0153698P.  
 PA (ENTRE-) ENTREMED INC.  
 XX Liang H, Sim KL, Chang-Murad A, Zhou X, Madsen J, Boerner RJ;  
 PI Bernejo IL, Mistry FR, Shepard SR, Schrimsher JI;  
 XX WPI; 2001-244802/25.



QY 121 GGGCTGGCGGACCTTCGCGCTTCTGCTGCGCCCTGAGAGACCTGTAAGCATC 180  
 DB 121 GGGCTGGCGGACCTTCGCGCTTCTGCTGCGCCCTGAGAGACCTGTAAGCATC 180  
 QY 181 GTGGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
 DB 181 GTGGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
 QY 241 CCCAGCTGGAGGCTGTGTTCTCAAGGCTCTGAAGGCTCGCTGAAGCCCGGCGACG 300  
 DB 241 CCCAGCTGGAGGCTGTGTTCTCAAGGCTCTGAAGGCTCGCTGAAGCCCGGCGACG 300  
 QY 301 TTCTCTTTTGAAGGACGCTCTGAGGACCTTCTGCGCGCGCGCGCGCGCGCGCG 360  
 DB 301 TTCTCTTTTGAAGGACGCTCTGAGGACCTTCTGCGCGCGCGCGCGCGCGCGCG 360  
 QY 361 CATGCTCTGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
 DB 361 CATGCTCTGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
 QY 421 GAGGCTCTGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 DB 421 GAGGCTCTGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 QY 481 AGTGGCGGAGCTGCTCAACGCTCAACGCTCAACGCTCAACGCTCAACGCTCAAC 540  
 DB 481 AGTGGCGGAGCTGCTCAACGCTCAACGCTCAACGCTCAACGCTCAACGCTCAAC 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546

RESULT 7  
 AA35375  
 ID AA35375 standard; DNA; 552 BP.  
 AC AAX35375;  
 XX 16-JUL-1999 (first entry)  
 DT XX  
 DE SEQ ID 50 of W09916889.  
 XX  
 XX Angiostatin; endostatin; interferon; thrombospondin;  
 KM interferon-inducible protein; platelet factor 4; anti-angiogenic;  
 KM anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;  
 KM diabetic retinopathy; macular degeneration; arthritis;  
 KM tumor cell production; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX W09916889-A1.  
 PN  
 XX 08-APR-1999.  
 PD  
 XX 30-SEP-1998; 98MO-US020464.  
 PF  
 XX 01-OCT-1997; 97US-00606099.  
 PR  
 XX (SEAR) SEARLE & CO G. D.  
 PA  
 XX Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;  
 PI McKearn JP;  
 XX  
 XX WPI; 1999-255098/21.  
 DR  
 XX  
 XX New multifunctional proteins useful for treating angiogenic-mediated  
 PT diseases.  
 DE  
 XX  
 XX Disclosure; Page 85; 121pp; English.  
 PS  
 XX The specification describes multifunctional proteins which comprise  
 CC combinations of angiostatin, endostatin, interferon, thrombospondin,  
 CC

CC interferon-inducible protein and platelet factor 4, and have anti-  
 CC angiogenic and/or anti-tumor activity. The multifunctional protein may  
 CC exhibit useful properties such as having similar or greater biological  
 CC activity when compared to a single factor or by having improved half-life  
 CC or decreased adverse side effects, or a combination of these properties.  
 CC The proteins can be used for treating an angiogenic-mediated disease,  
 CC e.g., cancer, diabetic retinopathy, macular degeneration, or arthritis.  
 CC They can also be used for inhibiting the production of tumor cells  
 CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,  
 CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)  
 CC in a patient and for inhibiting tumor growth. The present sequence is  
 CC used in the course of the invention  
 XX  
 SQ Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 546; DB 2; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-102;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACTTCAGCGGCTCTCCAGCTGTTGCGCTGTAAGGCGCGCTGTA 60  
 DB 1 CACAGCCACCGGACTTCAGCGGCTCTCCAGCTGTTGCGCTGTAAGGCGCGCTGTA 60  
 QY 61 GCGCGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
 DB 61 GCGCGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
 QY 121 GGGCTGGCGGCGACCTTCGCGGCTTCTGCTGCTGCGGCTGCGAGGACCTGTAAGCATC 180  
 DB 121 GGGCTGGCGGCGACCTTCGCGGCTTCTGCTGCTGCGGCTGCGAGGACCTGTAAGCATC 180  
 QY 181 GTGGCGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 DB 181 GTGGCGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 QY 241 CCCAGCTGGAGGCTGTGTTCTCAAGGCTCTGAAGGCTCGCTGAAGCCCGGCGACG 300  
 DB 241 CCCAGCTGGAGGCTGTGTTCTCAAGGCTCTGAAGGCTCGCTGAAGCCCGGCGACG 300  
 QY 301 TTCTCTTTTGAAGGACGCTCTGAGGACCTTCTGCGCGCGCGCGCGCGCGCGCG 360  
 DB 301 TTCTCTTTTGAAGGACGCTCTGAGGACCTTCTGCGCGCGCGCGCGCGCGCGCG 360  
 QY 361 CATGCTCTGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
 DB 361 CATGCTCTGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
 QY 421 GAGGCTCTGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 DB 421 GAGGCTCTGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 QY 481 AGTGGCGGAGCTGCTCAACGCTCAACGCTCAACGCTCAACGCTCAACGCTCAAC 540  
 DB 481 AGTGGCGGAGCTGCTCAACGCTCAACGCTCAACGCTCAACGCTCAACGCTCAAC 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546

RESULT 8  
 AAA68203  
 ID AAA68203 standard; cDNA; 552 BP.  
 AC AAA68203;  
 XX  
 XX 27-OCT-2000 (first entry)  
 DT XX  
 DE Human endostatin cDNA sequence.  
 XX  
 XX Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;  
 KM endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;  
 KM psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;  
 KM



KM	cerebral collateral; arteriovenous malformation; rubecosis; cancer;
KW	diabetic retinopathy; arthritis; wound healing; peptic ulcer;
XX	Helicobacter related disease; fracture; cat scratch fever; ss.
OS	
XX	Homo sapiens.
XX	
PN	WO200032631-A2.
XX	
PD	08-JUN-2000.
XX	
XX	06-DEC-1999; 99WO-US028897.
PF	
PR	04-DEC-1998; 98US-00206059.
XX	
PA	(ENTR-) ENTREMED INC.
XX	
P1	Macdonald NJ, Sim KL;
XX	
DR	WPI; 2000-412290/35.
XX	
XX	
PT	New angiogenesis-inhibiting protein receptors, useful in methods for
PT	treating diseases and processes that are mediated by angiogenesis, such
PT	as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.
XX	
PS	Disclosure; Page 86; 100pp; English.
XX	

This invention relates to angiogenesis-inhibiting protein receptors, and the DNA sequences encoding them. Angiogenesis is the generation of new blood vessels into a tissue, and normally occurs in wound healing, foetal development and embryonal development and the formation of the corpus luteum, endometrium and placenta. Angiostatin is a protein (see AB16450 and AA568202) involved in angiogenesis, and has an amino acid sequence similar to that of a plasminogen fragment (see murine plasminogen AB164940). Angiostatin has the ability to inhibit angiogenesis. Angiostatin is also an angiogenesis inhibiting protein (see AB16451 and AA568203). Sequences AA568242 and AB16522 represent coding and protein sequences of human laminin. Laminin is an angiostatin binding protein, and some of the peptides of the invention share homology with regions of laminin. Peptides AB16451-B16521 (excluding AB16490) are the angiogenesis-inhibiting protein receptor fragments of the invention. The peptides bind either angiostatin or endostatin and can be used in methods for treating diseases and processes that are mediated by angiogenesis, such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis, Crohn's disease, cerebral collateral, arteriovenous malformations, rheusitis, diabetic retinopathy, arthritis, wound healing, peptic ulcers, helicobacter related diseases, fistures, placental and cat scratch fever. They are useful for the detection and prognosis of cancer. DNA sequences A628204-A628241 encode the peptides of the invention

Query Match	100.0%;	Score 546;	DB 3;	Length 552;
Best Local Similarity	100.0%;	Pred. No. 5.1e-102;		
Matches 546;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 CACACCCACCGGCACTTCCAGCGGATGCTCCAGCCGTGGCTCAAGACCCCTGTCA 60  
Db 1 CACGCCACCGGCACCTTCCAGCCGATCTCCACCTGGATTGGCTCAACGCCCCCTGTCA 60  
QY 61 GCGGCGATGCGGGGCACTCCGGGGGCGCACTTCCAGTCTTCCAGCAGGGCGGGGCGGTG 120  
Db 61 GCGGCGATGCGGGGCACTCCGGGGGCGCACTTCCAGTCTTCCAGCAGGGCGGGGCGGTG 120  
QY 121 GGGGTGGCGGGGCACTTCCGCGCTTCTGTCCTTGAGCGCTGAGGAGCACTGTAAAGATC 180  
Db 121 GGGGTGGCGGGGCACTTCCGCGCTTCTGTCCTTGAGCGCTGAGGAGCACTGTAAAGATC 180  
QY 181 GTGCGCGGTCCGACCGCGAGCGCGGCCATCGTCAACTCAAGAGAGAGCACTGCTGTT 240  
Db 181 GTGCGCGGTCCGACCGCGAGCGCGGCCATCGTCAACTCAAGAGAGAGCACTGCTGTT 240  
QY 241 CCGAGCTGAGGCTCTTCTCAGGCTCTAGGGTCCGCTTGAAGCCCGGGGCAAGCATC 300  
Db 241 CCGAGCTGAGGCTCTTCTCAGGCTCTAGGGTCCGCTTGAAGCCCGGGGCAAGCATC 300

Db	241	CCAGAGTGGAGAGCTGTGTCTCAGGCTCTGAGAGGTCCGCTGAAGACCCGGGAGCAAGCATC	300
Qy	301	TTTCTCTTTGAACGGCAAGACGTCTCTGAGGCAATCCCACTGGTCCCAAGAGAGCTGTGG	360
Db	301	TTTCTCTTTTAAACGGCAAGAGAGTCTGAGAGGACCCCACTGGTCCCAAGAGAGCTGTGG	360
Qy	361	CATGAGCTGGACCCCAACGGGACGAGGCTGAACGAGAGCTACCTGAGAGAGCTGGGAGACG	420
Db	361	CATGAGCTGGACCCCAACGGGACGAGGCTGAACGAGAGCTACCTGAGAGAGCTGGGAGACG	420
Qy	421	GAGGCTCTCCCTCTGGGCTACGGGCTCAAGGCTCTCTGGCTGGGAGGACAGCTCTTGGGAGG	480
Db	421	GAGGCTCTCCCTCTGGGCTACGGGCTCAAGGCTCTCTGGCTGGGAGGACAGGCTCTTGGGAGG	480
Qy	481	AGTACCGCGAGCTGGCATCAGGCTACATCGTGCTGGGATTTGAGAACAGACTTCAATGACT	540
Db	481	AGTACCGCGAGCTGGCATCAGGCTACATCGTGCTGGGATTTGAGAACAGACTTCAATGACT	540
Qy	541	GGCTTC	546
Db	541	GGCTTC	546

ID	AAC62023 standard; DNA, 552 BP.
XX	
AC	AAC62023;
XX	
DT	06-MAR-2001 (first entry)
XX	
DE	Nucleotide sequence of human endostatin encoded by plasmid pWALCH#15.
XX	
KW	Streptomyces sp., strain C5; Smph; S. venezuelae; alpha-amylase; endostatin; cancer; tumour growth; angiogenesis; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	CDS
FT	1..552
FT	/tag= a
FT	/product= "endostatin"
PN	M020060945-A1.
PD	19-OCT-2000.
PX	
PF	12-APR-2000; 200OMC-USO09747.
PR	13-APR-1999; 99US-0129084P.
PA	(MERL ) MERCK & CO INC.
XN	
EI	Dasantl CL, Strohl WR,
DR	WFJ; 2000-686970/67.
DR	P-PDB; AAB30493.
XX	
PT	Preparation of soluble recombinant endostatin involves transforming <i>Streptomyces</i> host with expression vector comprising nucleotide sequence encoding endostatin operably linked to linker and leader peptide.
XX	
Example 1; Fig 6; 57pp; English.	
CC	The present sequence encodes human endostatin. The protein is expressed in streptomycetes. Leader sequences of Streptomyces sp., strain C5 Smph and S. venezuelae alpha-amylase proteins are linked to the N-terminal of endostatin. This ensures that endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer, inhibition of tumour growth, inhibition of angiogenesis, isolation of receptors for

```
Query Match      100.0%; Score 546; DB 3; Length 552;
Best Local Similarity 100.0%; Pred. No. 5.1e-102;
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 301 TTCTCCTTTGACGGCAAGGACGTCTCTAGGCACCCCACTTGGCCCCAGAGAAGCGTGTGG 360

Ph 301 TTCTCCTTTGACGGCAAGGACGTCTCTAGGCACCCCACTTGGCCCCAGAGAAGCGTGTGG 360

QY 541 GCCTCC 546  
|||||  
Db 541 GCCTCC 546

AC AAC88289;

DT 02-MAR-2001 (first entry)

aa	DE	Human endostatin coding sequence	SEQ ID NO: 1
1		ATG	1
2		CTG	2
3		CTG	3
4		CTG	4
5		CTG	5
6		CTG	6
7		CTG	7
8		CTG	8
9		CTG	9
10		CTG	10
11		CTG	11
12		CTG	12
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35		CTG	35
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37		CTG	37
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40		CTG	40
41		CTG	41
42		CTG	42
43		CTG	43
44		CTG	44
45		CTG	45
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98		CTG	98
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103		CTG	103
104		CTG	104
105		CTG	105
106		CTG	106
107		CTG	107
108		CTG	108
109		CTG	109
110		CTG	110
111		CTG	111
112		CTG	112

XX Endostatin; antiangiogenic; angiogenesis; human; mouse; cancer  
 KW inflammation; angiogenesis-dependent disease; ds.  
 KM inflammation; angiogenesis-dependent disease; ds.

OS Homo sapiens.

PN WO2000067771-A1.

PD 16-NOV-2000

XX

PF 02-MAY-2000; 2000MO-US012063  
XX  
PR 06-MAY-1999; 99US-0132907P  
PR 14-JUL-1999; 99US-00353333  
XX  
PA (BURN-) BURNHAM INST.

PI Vuori K;

DR WPI; 2001-040937/05.  
DR P-PSDB; AAB49379.

Endostatin peptide comprising at least four endostatin amino acid

PT diabetic retinopathy

PS Disclosure; Page 111-112; 146pp; English

The present invention provides endostatin peptides which can be used in the modulation of angiogenesis. This is useful in the treatment of cancer, inflammation, rheumatoid arthritis, chronic articular rheumatism, psoriasis, disorders associated with inappropriate invasion of vessels such as diabetic retinopathy, neovascular glaucoma, retinopathy of prematurity, macular degeneration, corneal graft rejection, retrolental fibroplasia, rubeosis, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent diseases include Osler-Weber syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilic joints and wound granulation. In addition, the peptides can be used as birth control agents

aa	Sequence	552 BP;	83 A;	196 C;	179 G;	94 T;	0 U;	0 Other
sq								

Query Match	100.0%;	Score 546;	DB 5;	Length 552;
Best Local Similarity	100.0%;	Pred. No. 5.1e-102;		
Matches 546;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 CAAGCAGCGGCACTTCCAGGCGGTCTCCACTTGTTGTGGCTCAACAGGCCCCCTGTCA 60

Db 1 CACAGCGACCGGCACTTCCAGGCGGTCTCCACTTGTTGTGGCTCAACAGGCCCCCTGTCA 60

61 GGCGGATGCGGGGATCCGGGGGCGGACTTCAGTGCCTTCAGCAGGCGCGGGCCGTG 12

121 GGGCTGGCGGACCTTCCGCGCTTCTCTCGCGCTGAGGACCTGTACAGATC 1

Db 121 GGGCTGGCGGGACCTTCCGCGCCCTCTGCTCCCTCGCGCTGAGAGCCGTAACAGCATC 1

Dy 181 GTCGCGCTGCGGACCGCGGAGCGCGGCCATGTCACCTCAAAGACGCTGTGTTT 2

181 GAGCGCGTGCAGCCGCGGACGCCGTCATCGTCAACCTCAGAGACGAGCTGCTGTTT 2

QY	241
CCGAGCTGGGAGGCGCTGTTCTCAGGCTCAGAGGATCCGTTGAAGCCCGGGGCAAGCATC	3

DQ  
301 TTCTCCTTTGACGGCAAGACCTCTGAGGACCCCACTTGCCCCAGAAGAGCGGTGG 3

DB  
301 TTTCTCTTTTGAAGGCAAGACCTCTGAGGACCCCACTTGCCCCAGAAGAGCGGTGG 3

[illegible]

**D**

db	361	CATGGCTCGGACCCCAAGCAGGCAGAGCATGAACAAGAATTTGTAAATAAATTTCCTTCCCCTTGTAATGTTG
	QY	421 GAAGCTCCCTCGGCCAACGGGACCAGGCTCTTAGCTGCTGGGGCACGACTTGGGGCAG  4

Db 421 GAGGCTCCCTCGGCCACGGGCCAGGCTCCTGCGTGTGGGGGGCAGGCTCTGGGGCAG 4  
481 AATTGCTGGAGCTTGCCATCAGCGCTACATCGTGTCTTGCAATTGAGAACAGCTTCATGACT 5

481 AGTCCCGAGCTGCCATCAGCCTACTCGCTCTGCATTGAGAACAGCTTCATGACT 5

100

! I NOW T5

PI Zhou Y;

PI Zhou Y;



```

Db 427 GAGGCTCCCTCGGCGCAGGCGCTCTGCTGCTGCGGGGCGAGGCTTCTTGGGCGAG 486
Qy 481 AGTCCGCGGAGCTGCTCATCAGCGCTCATCTGCTCTGCAATTGAGAACAGCTTCATGACT 540
Db 487 AGTCCGCGGAGCTGCTCATCAGCGCTCATCTGCTCTGCAATTGAGAACAGCTTCATGACT 546
Qy 541 GCTTCC 546
Db 547 GCTTCC 552

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## RESULT 14

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AAZ08750
ID AAZ08750 standard; cDNA, 563 BP.
XX
AC AAZ08750;
XX
DT 03-NOV-1999 (first entry)
XX
DE Human endostatin cDNA isolate pMON20440.
XX
KW Endostatin; inclusion body; expression; anticancer; antimetastatic;
KW angiogenesis; migration; proliferation; inhibition; collagen XVIII;
KW tumour; ss.
XX
OS Homo sapiens.
XX
PN W09942486-A1.
XX
PD 26-AUG-1999.
XX
PF 19-FEB-1999; 99WO-US003271.
XX
PR 23-FEB-1998; 98US-0075587P.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Harding EI, Vieland BN;
XX
DR WPI; 1999-527458/44.
XX
PT Production of endostatin by refolding recombinant protein, useful as
PT anticancer and antimetastatic agent.
XX
PS Claim 49; Page 47-48; 52pp; English.
XX

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```

CC A method has been developed for the production of endostatin (I). The
CC method comprises: (i) culturing host cells expressing the gene for (I);
CC (ii) recovering the gene product; (iii) refolding it at near neutral pH;
CC and (iv) isolating properly folded (I). (i) are inhibitors of
CC angiogenesis, by inhibiting migration and proliferation of endothelial
CC cells. The method is used to produce human or murine (I) from inclusion
CC bodies formed in recombinant bacteria. (i), the C-terminal fragment of
CC type alpha 1 collagen XVIII, is known to inhibit growth of some
CC metastases and primary tumours. The present sequence represents a cDNA
CC isolate containing a PCR fragment encoding human endostatin, including
CC the native human collagen XVIII C-terminal region
XX
SQ Sequence 563 BP; 87 A; 198 C; 181 G; 97 T; 0 U; 0 Other;

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```

Query Match 100.0%; Score 546; DB 2; Length 563;
Best Local Similarity 100.0%; Pred. No. 5, 1e-102;
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CACAGCCACCGGAGCTTCGAGCGGCTGCTCAAGCTGTTGCGCTCAACAGCCCTCTGCA 60
Db 6 CACAGCCACCGGAGCTTCGAGCGGCTGCTCAAGCTGTTGCGCTCAACAGCCCTCTGCA 65
Qy 61 GCGCGCATGCGGGGCGATCCGCGGGGCGGAGCTTCAGTCTTCAGAGAGCGCGGCGGCTG 120
Db 66 GCGCGCATGCGGGGCGATCCGCGGGGCGGAGCTTCAGTCTTCAGAGAGCGCGGCGGCTG 125

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Qy 121 GAGGCTCCCTCGGCGCAGGCGCTCTGCTGCTGCGCGCTGCAAGACCTTGATACGATC 180
Db 126 GAGGCTCCCTCGGCGCAGGCGCTCTGCTGCTGCGCGCTGCAAGACCTTGATACGATC 185
Qy 181 GTGCGCGCTGCGGAGCGCGCAGCGCTGCTGCTGCAAGACCTTGATACGATC 240
Db 186 GTGCGCGCTGCGGAGCGCGCAGCGCTGCTGCTGCAAGACCTTGATACGATC 245
Qy 241 CCCAGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 246 CCCAGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
Qy 301 TTCTCTTTTTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 306 TTCTCTTTTTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 365
Qy 361 CATGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 366 CATGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 425
Qy 421 GAGGCTCCCTCGGCGCAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 426 GAGGCTCCCTCGGCGCAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
Qy 481 AGTCCGCGGAGCTGCTCATCAGCGCTCATCTGCTCTGCAATTGAGAACAGCTTCATGACT 540
Db 486 AGTCCGCGGAGCTGCTCATCAGCGCTCATCTGCTCTGCAATTGAGAACAGCTTCATGACT 545
Qy 541 GCTTCC 546
Db 546 GCTTCC 551

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## RESULT 15

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ID AAA64013
AC AAA64013 standard; DNA, 816 BP.
XX
AC AAA64013;
XX
DT 20-DEC-2000 (first entry)
XX

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DE DNA encoding a human angiogenesis inhibitor designated KED.
XX
KW Angiogenesis inhibitor; KED; kringe protein; angiogenesis; tPA;
KW tissue plasminogen activator; tumour; atherosclerosis; arthritis;
KW retinopathy; bronchial vascular congestion; inflammatory bowel disease;
KW adult respiratory distress syndrome; Castleman's disease; psoriasis;
KW hepatitis; aneurysm; renal disease; haemangioma; ss.
XX
OS Homo sapiens.
XX

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FH Key Location/Qualifiers
FT CDS 1..816
FT /*tag = a
FT /product = "angiogenesis inhibitor KED"

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PN W0200049871-A1.
XX

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PD 31-AUG-2000.
XX

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PF 24-FEB-2000; 2000WO-US004798.
XX

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PR 24-FEB-1999; 99US-0121341P.
XX

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PR 25-FEB-1999; 99US-0121633P.
XX

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PR 18-NOV-1999; 99US-016176P.
XX

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PA (FORD-) FORD HEALTH SYSTEM HENRY.
XX

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PI Dou D, Chopp M, Wang L, Mikkelsen T;
XX

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DR WPI; 2000-572016/53.
XX

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DR P-PSDB; AAB08407.
XX

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PT Use of kringle protein and kringle derived from plasminogen and  
PT composition comprising kringle proteins for treating tumor and  
PT atherosclerosis, arthritis and retinopathy.

PS Disclosure, Page 151; 163pp; English.

XX The present sequence encodes a human polypeptide which is a potent  
CC angiogenesis inhibitor, designated KED. The KED polypeptide, kringle  
CC proteins, or a kringle derived from human tissue plasminogen activator  
CC (tPA) protein are used to inhibit angiogenesis. Kringle protein, KED or  
CC tPA are useful for treating tumours, as well as atherosclerosis,  
CC arthritis, retinopathy and other similar diseases. KED is also useful for  
CC the treatment of diseases such as bronchial vascular congestion,  
CC inflammatory bowel disease, adult respiratory distress syndrome,  
CC Castleman's disease, psoriasis, hepatitis, aneurysm, renal disease and  
CC haemangioma

XX Sequence 816 BP; 156 A; 259 C; 254 G; 147 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 3; Length 816;

Best Local Similarity 100.0%; Pred. No. 5.2e-102; Indels 0; Gaps 0;

Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CACAGCCACGCGCAGCTTCCAGCGGCTGCTCCAGCTGCTGCTCAACAGCCCTCTGTCA 60
DB 265 CACAGCCACGCGCAGCTTCCAGCGGCTGCTCCAGCTGCTGCTCAACAGCCCTCTGTCA 324
QY 61 GAGGCGATGCGGGGATCGCGGGGCGCATCTTCCAGTCTTCAGCAGGCGCGGCGCTG 120
DB 325 GAGGCGATGCGGGGATCGCGGGGCGCATCTTCCAGTCTTCAGCAGGCGCGGCGCTG 384
QY 121 GAGCTGCGGGGACCTTCCGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 385 GAGCTGCGGGGACCTTCCGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
QY 181 GTGCGCGGCTGCGCAGCGCGGCTGCGCAGCTGCTCAACCTCAAGAGAGAGCTGCTGTT 240
DB 445 GTGCGCGGCTGCGCAGCGCGGCTGCGCAGCTGCTCAACCTCAAGAGAGAGCTGCTGTT 504
QY 241 CCCAGCTGAGAGGCTGTTCTGAGGCTCTGAGGCTCGCTGAGGCTCGGCGGCGAGCGCATC 300
DB 505 CCCAGCTGAGAGGCTGTTCTGAGGCTCTGAGGCTCGCTGAGGCTCGGCGGCGAGCGCATC 564
QY 301 TTCTCTTTGAGCGCAGAGAGCTGCTGAGGAGCAACCCACCTGAGGCTGAGAGAGCTGTGG 360
DB 565 TTCTCTTTGAGCGCAGAGAGCTGCTGAGGAGCAACCCACCTGAGGCTGAGAGAGCTGTGG 624
QY 361 CATGCTGCGAGCCCAACGAGGCGCAGGCTGACCGAGAGCTACTGTGAGACGTGCGGAGC 420
DB 625 CATGCTGCGAGCCCAACGAGGCGCAGGCTGACCGAGAGCTACTGTGAGACGTGCGGAGC 684
QY 421 GAGGCTGCTGCGGCGCAGGCTGCTGCGGCTGCTGCGGCGGCGAGGCTCTTGGGCGAG 480
DB 685 GAGGCTGCTGCGGCGCAGGCTGCTGCGGCTGCTGCGGCGGCGAGGCTCTTGGGCGAG 744
QY 481 AGTGCAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 745 AGTGCAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804
QY 541 GCTCTCC 546
DB 805 GCTCTCC 810
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Search completed: September 15, 2004, 18:50:09  
Job time : 338 secs